Search completed: December 8, 2003, 09:55:35 Job time : 6.8 secs

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December 8, 2003, 09:46:14; Search time 3.81143 Seconds (without alignments) 357.812 Million cell updates/sec Run on:

US-09-938-114-3 Title: Perfect score:

170 1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5 Searched:

127863 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Post-processing: Minimum Match 0%

Listing first 45 summaries

SwissProt 41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Descripti	P81509 crotalus ho	P23807 trimeresuru			111			trimeresur			P81113 trimeresuru							crotalus	gallus ga		P16112 homo sapien				Q61282 mus musculu				_		P49260 orvetolams	Н	32 pos	
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TXB TRIFL STANDARD; PRT; 146 AA P23807; Q91247; 01-NOV-1991 (Rel. 20, Created) 15-JUL-1998 (Rel. 36, Last sequence update)

RESULT 2 IXB TRIFL ID IXB TI AC P2380 DT 01-NO'DT

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P55068 rattus norv Q28062 bos taurus P27812 mus musculu Q90953 gallus gall P06027 anthocidari Q28858 macaca neme Q9erb4 rattus norv Q62059 mus musculu P81282 bos taurus P13611 homo sapien Q9m2j7 macaca mula	P26718 homo sapien
PGCB_RAT PGCB_BOVIN NK12_MOUSE PGCV_CHICK LECE_ANTCR PGCV_MACNE PGCV_MOUSE PGCV_MOUSE PGCV_HOMAN PGCV_HOMAN NKGD_MACMOUSE	NKGD_HUMAN
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ALIGNMENTS

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TISSUBE-Venom;

RX MEDIJINE=96420502; PubMed=8823201;

RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,

Randrews R.K., Kroll M.H., Berndt M.C.;

Smith A.I., Lopez J.A., Berndt M.C.;

RT "Binding of a novel 50-kilodalon alboaggregin from Trimeresurus

R1 albolabris and related viper venom proteins to the platelet membrane

RT glycoprotein ID-IX-V complex. Effect on platelet aggregation and

RT glycoprotein ID-mediated platelet activation.";

RL Blochemistry 35:12629-12639(1996).

CC --- FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VMF

CC --- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.

CC --- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.

CC --- SUBUNIT: Contains I C-type lectin family domain.

SMART; SM00034; CLECT; I.

DR RROSITE; PS50041; C_TYPE_LECTIN_2; I.

PROSITE; PS50041; C_TYPE_LECTIN_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CHG-ED beta subunit.
Crotalus horridus horridus (Timber rattlesnake).
Crotalus horridus (Timber rattlesnake).
Crotalus seazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
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                                 PRT;
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                                  STANDARD;
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Р81509;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=9731317; PubMed=9187649;
Mizuno H., Frijimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
                                                                                                                                       MEDLINE-96184662; PubMed=8645314;
Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
"cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAGULATION FACTOR IX/FACTOR X-BINDING
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                  Atoda H., Hyuga M., Morita T.; "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis.
           Coagulation factor IX/factor X-binding protein B chain precursor
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INTERCHAIN (WITH C-102 OF A BY SIMILARITY.
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-i- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                protein from snake venom.";
Biochem. Biophys. Res. Commun. 220:382-387(1996).
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(Rel. 42, Last annotation update)
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PDB; 1IXX; 06-MAY-98.
PDB; 1BJ3; 16-AUG-99.
INCEPPC; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMARY; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                         immunoglobulin E.";
J. Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                  MEDLINE=91332000; PubMed=1831197;
                                       Trimeresurus flavoviridis (Habu)
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15-Jul. 1998 (Rel. 36, Last sequence update)
15-Jul. 1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 4.
Trimeresurus albolabris (White-lipped pit viper)
Trimeresurus albolabris (White-lipped pit viper)
Lepidosauria; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 131; DB 1; Length 123;
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MEDLINE=98189535; PubMed=9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23807; 1IXX.
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                                                                                                                                                                                                                                                         16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelets.";
Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor
agglutination.
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Pred. No. 1.1e-10;
2; Mismatches 6
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InterPro; IPR001304; Lectin_C.
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96184662; PubMed=8645114;
Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
"CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
protein from snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of C-type lectin domains.";

Nat. Struct. Biol. 4:438-441(1997).

-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.

-!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97331317; PubMed=9187649;
Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.,
"Structure of coagulation factors IX/X-binding protein, a heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN A CHAIN.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                  P23806; Q91246;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor IX/factor X-binding protein A chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91332000; PubMed=1831197;
Atoda H., Hyuga M., Morita T.;
"The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homology with asialoglycoprotein receptors, proteoglycan core
protein, tetranectin, and lymphocyte Fc epsilon receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3iochem. Biophys. Res. Commun. 220:382-387(1996)
                                                                        152 AA
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PIR, JC4690, JC4690.
PDB, 11XX, 06-MAY-98.
INCEPPO, IPR001304; Lectin C.
INCEPPO; IPR001304; Dencratis_ac.
PRINTS; PR01504; PROFEATING.; 1.
PRINTS; PR01504; PROFEATING.; 1.
PROSITE; PS00015; C_TYPE_LECTIN 1; 1.
PROSITE; PS00041; C_TYPE_LECTIN 1; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 266:14903-14911(1991).
                                                                        PRT;
                                                                                                                                                                                                                                                                             Trimeresurus flavoviridis (Habu)
                                                                     STANDARD;
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36
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                                                                  TRIFL
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RESULT 4

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DT 01-NO
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Thromb. Haemost. 79:609-613(1998)
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INTERCHAIN (WITH C-98 OF B CHAIN). BY SIMILARITY.
                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Venom,
MEDIATE-984189535, PubMed=9531050;
MEDIATE-98489535, PubMed=9531050;
KOWALSKA M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                         Length 152;
                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                    17213 MW; FB3DDD2369009263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disulfide-linked.
-!-SUMLELLULAR LOCATION: Secreted.
-!-SIMILARLY: Contains 1 C-type lectin family domain.
HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B3569F5BF91F6624 CRC64;
                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 1.
Trimeresurus albolabris (White-lipped pit viper)
                                                                                                                                                                                                                       Score 123; DB 1;
Pred. No. 2.3e-09;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                               131 AA.
                                                                                                                                                                                                                                                          DCSSDWSSYEGHCYKVFKQSKTWTDAE 27
                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                       24 DCLSGWSSYEGHCYKAFEKYKTWEDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15427 MW;
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20; Conservative
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1002
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13
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152 AA;
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102
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ID ABA1_TRIAB
AC P81111;
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125 AA; 15037 MW; 1ED2027ED817FCA0 CRC64;

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                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH C-80 IN ALPHA CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                              Bothrops jararaca (Jararaca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93157385; PubMed-8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
Titani K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G., Liddington R.C.;
                                              0
         Score 120; DB 1; Length 131;
Pred. No. 4.9e-09;
5; Mismatches 5; Indels
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-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                               Botrocetin, beta chain (Platelet coagglutinin).
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PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
70.6%; Scor.
65.5%; Pred. No. 4...
5; Mismatches
                                                                                                                                                                                                                   125 AA.
                                                                                                        1 DCPSDWSSYDQYCYRVFKRIQTWEDAERF 29
                                                                                     1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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                                                                                                                                                                                                                                                                                                                                                                               Viperidae; Crotalinae; Bothrops.
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                               Local Similarity 65.5
hes 19; Conservative
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75
113
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PDB; IIJK; 17-JUL-02.
PDB; IFVU; 14-FEB-01.
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75
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P22030;
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Matches
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MEDLINE=91129280; PubMed=1993206;
MEDLINE=91129280; PubMed=1993206;
Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
Fukui H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical characterization of two structurally and functionally distinct forms of botrocetin, the platelet coagglutinin isolated from the venom of Bothrops jararaca.";
Biochemistry 30:1957-1964(1991).
                                                     Gaps
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"Primary Structure of two-chain botrocetin, a von Willebrand factor medulator purified from the venom of Bothrope jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
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                                                                                                                                                                                                                                                                                                                       01-AUG'1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 42, Last sequence update)
Bornocetin, alpha chain (Platelet coagglutinin).
Botrocetin, alpha chain (Platelet coagglutinin).
Botrocetin, Alpha chain (Platelet Caniata, Vertebrata; Euteleostomi; Lepidosauria, Squamata; Soleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
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MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93157285; PubMed-8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                   0
70.0%; Score 119; DB 1; Length 125; 65.5%; Pred. No. 6.3e-09; ive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                133 AA.
                                                                                                    1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
Lectin; 3D-structure.
                                                                                                                                                                                                                                                                                PRT;
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PDB; 11JK; 17-JUL-02.

PDB; 1FWU; 14-FEB-01.

InterPro; IPR002353; Antifreezell.

InterPro; IPR001304; Lectin C.

Pfam; PF00059; lectin C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND DISULFIDE BONDS.
       Query Match
Best Local Similarity 65.55
Matches 19; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
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BY SIMILARITY.
                                    INTERCHAIN (WITH C-75 IN BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost.
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crocalinae, Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alboaggregins A and B. Structure and interaction with human platelets.";
                                                                                                     Length 133,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
TISSUB=Venom;
MEDLINE=98189535; PubMed=9531050;
Kowalaka M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 116; DB 1; Length 11
Pred. No. 1.5e-08;
3; Mismatches 7; Indels
 128
80 INTERCHAIN (WITH C-75 IN B
1200
15215 MW; E4CF4502946AC74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       059EDFF6B474C4CE CRC64;
                                                                                                  68.8%; Score 117; DB 1; Lv 65.5%; Pred. No. 1.2e-08; live 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093427;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Convulxin beta precursor (CVX beta).
                                                                                                                                                                                                                                                                                            118 AA.
                                                                                                                                                                   1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                        1 DCPSGWSSYEGNCYKFFQQKMWADAERF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thromb. Haemost. 79:609-613(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 AA; 13794 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 68.2%;
l Similarity 65.5%;
19; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                       Alboaggregin B beta subunit
                                                                                                                                     19; Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
13
75
                                                                  133 AA;
                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
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CVXB_CRODU
                                                                                                                                                                                                                                                     RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
Ebkaryota; Metazoa; Chordata; Csouth American rattlesnake).
Lepidosauria; Squamata; Craniata; Vertebrata; Euteleostomi;
Uppridosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
NCBI_TaxID=8732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Echis carinatus (Saw-scaled viper).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                  Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
aggregating protein from Crotalus durissus terrificus venom.";
Blochem. J. 333:389-393 (1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
-!- SUBUNIT: Heterohexamer of three alpha chains and three beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                        FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.2%; Score 116; DB 1; Length 148; 67.9%; Pred. No. 1.8e-08; .ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
94D7E3E1BC693B9F CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Echicetin beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONVULXIN BETA
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Pfam; PR00059; lectin c; 1.
SMART; SM0004; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Lectin; Glycoprotein; Signal.
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                                                                                                                                                                                                                                 TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
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MEDLINE=95091801; PubMed=7999097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chains; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 136 E
148 AA; 17402 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viperidae, Viperinae, Echis.
NCBI_TaxID=40353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
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les 19; Conser
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55
100
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P81996;
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SEQUENCE
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Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.
-!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
                                                                  -!- SIBCELLIAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 C-type lectin.
InterPro; 1PR001304; Lectin.C.
Pfam; PF00059; lectin.C; 1.
PROSITE; SM0004; CIECT; L.
PROSITE; PSS0041; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                    125 AA; 14798 MW;
                                                                                                                                                                                                                                                                         Best Local Similarity 62.1
Matches 18; Conservative
                                                                                                                                                                                             15
121
                                                            disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330
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32
98
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 platelets.";
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ABBA_TRIAB
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BY SIMILARITY.
INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY
Peng M., Holt J.C., Niewiarowski S.; "Isolation, characterization and amino acid sequence of echicetin beta subunit, a specific inhibitor of von Willebrand factor and thrombin interaction with glycoprofein Ib.", Biochem. Biophys. Res. Commun. 205:68-72(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                      ŏ
                                                                                                                                                                                                                                     Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby E.P.;
"Echicetin: a snake venom protein that inhibits binding of von
Willebrand factor and alboaggregins to platelet glycoprotein Ib.";
                                                                                                 MEDLINE=97250657; PubMed=9163349;
Polgar J., Magnenat B.M., Peitsch M.C., Wells T.N.C., Sagi M.S.A.,
Clemetson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PB1113;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
18-JUL-1998 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 3.
Trimeresurus albolabris (White-lipped pit viper).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                   "Amino acid sequence of the alpha subunit and computer modelling
the alpha and beta subunits of echicetin from the venom of Echis
carinatus (saw-scaled viper) ";
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 114; DB 1; Length 123; 62.1%; Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                             Blood 81:2321-2328(1993).
-!- FUNCTION: Binds to platelet GPIb and inhibits platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
PIR; JC2415, JC2415.
HSSP; P23807; 11XX.
InterPro; IPR001304; Lectin_C.
Pfam; PR00059; lectin_C.
Pfam; PR00059; Lectin_C.
PROSITE; PS00015; CIECT; 1.
PROSITE; PS00015; CIECT; 1.
PROSITE; PS00015; CITYPE_LECTIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C42COAD7CDE18CA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
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                                                                                                                                                                           Biochem. J. 323:533-537(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14869 MW;
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119
75
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                                                                                                                                                                                                                                                                                                     agglutination.
                                                                           SEQUENCE OF 1-30.
                                                                                                                                                                                                     CHARACTERIZATION
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30
75
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Length 125;

CAFA24C098DF3293 CRC64;

C-TYPE LECTIN (LONG FORM)

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

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                                                                               Gaps
                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Alboaggregin B alpha subunit.
Trimeresurus albolabris (White-lipped pit viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98189535; PubMed=9531050; Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J., Calvete J.J., Niewiarowski S.; "Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Heterodimer of alpha and beta subunits, di
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P28966; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH C-75 IN (BY SIMILARITY).
4798 mm,
66.5%; Score 113; DB 1; Le
'4. Pred. No. 3.8e-08;
8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                    132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                             1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                      DCPFGWSSYEGYCYKVYNKKMNWEDAESF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00059; Lectin C.
Pfam, PF00059; Lectin c.; 1.
SMART, SMOR34; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Βĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15419 MW;
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                                                                                                                                                                                                                                                                                    STANDARD;
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13
127
79
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132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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computer modelling of the venom of Echis

7

Matches

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INTERCHAIN (WITH C-75 IN BETA CHAIN) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Purification and characterization of a Ca2+ -dependent prothrombin activator, multactivase, from the venom of Echis multisquamatus."; J. Biochem. 122:991-997(1997).
-!- FUNCTION: Multactivase, a carinactivase-like calcium dependent prothrombin activator, activates prothrombin via recognition of the calcium ion bound conformation of its gamma-carboxyglutamic acid (GLA) domain
                             MEDLINE=97250657; PubMed=9163349;
Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Sagi M.S.A.,
Clemetson K.J.;
                                                                                                                                                                                                                         Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby B.P.,
"Echicetin: a snake venom protein that inhibits binding of von
Wilebrand factor and alboaggregins to platelet glycoprotein Ib.";
Blood 81:2321-2328 [1993].
-!- FUNCTION: Binds to platelet GPIb and inhibits platelet
agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: Composed of a catalytic subunit with metalloprotease activity and a regulatory subunit comprising two homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 102.5; DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: Heterodimer of alpha and beta subunits.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8F11C2D0BDC70B16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last amotation update)
Multactivase regulatory subunit (Fragment)
Echis multisquamatus (Central Asian sand viper)
                                                                               "Amino acid sequence of the alpha subunit and
the alpha and beta subunits of echicetin from
carinatus (saw-scaled viper).";
Biochem. J. 323:533-537(1997).
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PR0059; Lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCSSDWSSYEGHCYKVFKOSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                           MEDLINE=93244424; PubMed=8481512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
MEDLINE=98104052; PubMed=9443815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AA; 15803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.3%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viperidae, Viperinae, Echis.
NCBI_TaxID=93050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.00,
"hea 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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127
119
81
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                                                                                                                                                                        CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31
102
81
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                      MILINE-FOLLOW.

MEDLINE-FOLLOW.

MEDLINE-96420502; PubMed-8823201;

Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M., Smith A.I., Lopez J.A., Berndt M.C.;

Smith A.I., Lopez J.A., Berndt M.C.;

"Binding of a novel 50-kilodalton alboaggregin from Trimeresurus
albolabris and related viper venom proteins to the platelet membrane glycoprotein Ib-IX- complex. Effect on platelet aggregation and glycoprotein Ib-mediated platelet activation.";

Biochemistry 35:12629-12639(1996).

-I. FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding and stimulates agglutination.
-!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
-!- SUBCELDUIAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
SMART; SM00034; CLECT; 1.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-92 IN BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryos, metazoa; Chorateu viperi.
Lepidosauria; Squamata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Echis.
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                           0;
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                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BSDA100D383E3547 CRC64;
       Pred. No. 5.5e-08;
6; Mismatches 6;
                                                                                                                                                                                                                                                                                      Crotalus horridus horridus (Timber rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.3%; Score 111; DB 1;
ilarity 62.1%; Pred. No. 7.1e-08;
Conservative 3; Mismatches 8
                                                                                                                                                                                                                                   (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                    127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                           DCSSDWSSYEGHCYKVFKOSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DCSSDWSSYEGHCYKVFKOSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Echicetin alpha subunit.
Echis carinatus (Saw-scaled viper)
                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15162 MW;
   58.68;
                      Conservative
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
15
120
120
81
                                                                                                                                                                                                                                                                      CHH-B alpha subunit
Best Local Similarity
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tes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE=Venom;
                    17;
                                                                                                                                                                                                                                                   28-FEB-2003
                                                                                                                                                                                                                                    28-FEB-2003
                                                                                                                                                                                 CHBA CROHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECHA ECHCA
P81017;
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                 P81508;
                                                                                                                                              RESULT 13
CHBA_CROHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lectin.
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Best Loca Matches

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ECHCA RESULT 14 ECHA

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Gaps

1;

Indels

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Search completed: December 8, 2003, 09:53:10 Job time : 5.14476 secs

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December 8, 2003, 09:49:24; Search time 14.0857 Seconds (without alignments) 531.285 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                             1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                          US-09-938-114-3
                                                                                                                                                                                      Title:
Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 2000000000 Minimum DB g Maximum DB g

Total number of hits satisfying chosen parameters:

830525 seqs, 258052604 residues

Searched:

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_tungi:*
4: Sp_tungi:*
5: Sp_tungi:*
5: Sp_inwertebrate:*
8p_manmal:*
8p_manmal:* Bp_vertebrate:* sp_organelle:*
sp_phage:* sp_rodent:*
sp_virus:* sp_plant:* 9. 110.: 112: 141: .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp archeap:*

sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*

		Description	The cooperation of the cooperati									Q98sm5 agkistrodon	OBjiwl agkistrodon				U8J1V8 agkistrodon	O9bsm9 echis carin			ZOWIS ABAISLIOUON
SUMMARIES		ID	09IAM1	090889	031160	ORAVAA	OMATOC	COLABO	2011100	Santa Contract	(AT090)	QSSSMS	OBJIMI	09DG31	09T840	08.TTV9	041000	CALCANA	000860	090WL9	
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		Match Length DB	152	152	152	146	146	146	146	146	7 7 7	177	146	146	146	155	ייי	TOT	146	124	
•	Query	Match	95.9	91.2	91.2	87.1	80.0	78.8	78.2	78.2			9.//	74.7	72.9	72.9	72.4	7 1	72.4	71.2	
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à 셤 RESULT 2

Q9prq7 bothrops ia		Q9ygn4 agkistrodon				Q9prp7 echis carin						Ogneso trimorogy		Cologia agaisticach			Q8av98 trimeresuru	Q8jgt7 trimeresuru			08av97 trimeresum		P79787 Gallia				Ocaca agristicati	Oszeza Dos Laurus	
								09PS19					091841							69¥GQ	Q8AV97	Q9PS05	P79787	OBUVC6		_	С	09PSM4	Q9PRQ8
	123 13				30 13		Н	40 13	Н	Н	Н	40 13	136 13	154 13						157 13			2109 13				1 40	135 13	42 13
70.6	70.6	0.0		4.00	7.89	68.2	68.2	67.6	67.1	67.1	65.9	61.2	9.09	9.09	0 09		0.0	28.9	58.2	58.2	58.2	57.1	55.9	55.3	55.3	54.7	54.1	53.5	52.9
120	120	110	110	011	977	778	116	115	114	114	112	104	103	103	102	100	707	001					92	94	94	93	92	91	90
17	20 0	40	6.5	1 6	7 (62.0	24	25	26	27	28	29	30	31	32	3.5	0 0	# L	35	36	3.7	80	<u>რ</u>	40	41	42	43	44	45

ALIGNMENTS

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Tisous-recent.

Yu H.-X., Xiang K.-J., Liu J.;

Yu H.-X., Xiang K.-J., Liu J.;

"cDNA sequencing and analysis of eleven C-type lectin-like protein

"cDNA sequencing and acutus.";

"cDNA sequencing and acutus.";

"chin. J Biochem. Biophys. 0:0-0(2002).

"EMBL; API76420; AAF26286.2; -..

"R EMBL; API76420; AAF26286.2; -..

"R EMBL; API76420; AAF26286.2; -..

"R FAM; PRO0034; Lectin.C.

"P FAM; PRO0034; CLECT; 1.

"SMART; SM00034; CLECT; 1.

"R PROSITE; PS00615; C TYPE LECTIN.1; 1.

"PROSITE; PS00615; C TYPE LECTIN.1; 1.

"PROSITE; PS00611; C TYPE LECTIN.1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-UNA-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Agkisacutacin A chain.
Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Viperidae; Crotalinae; Deinagkistrodon.
Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.9%; Score 163; DB 13; Length 152; 96.6%; Pred. No. 1.5e-15; Live 0; Mismatches 1; Indels
                                       152 AA.
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Conservative
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=Venom;
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                                    Q9IAM1
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RESULT 1
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24 DCSSSWSSYEGHCYKAFKQSKTWADAESF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
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                                                                                              QBAYA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9IAMO
                                                                                QBAYA4
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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Q9IAM0
                                                      RESULT 4
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                                                                                                        Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
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                                                                                                                                                                                      SECUENCE FROM N.A.
TISSUB=Venom gland;
Ogawa T., Tani A.;
"Purification, Sequencing, and cDNA Cloning of a Heterodimeric Anticoagulant Protein from Agkistrodon actus Venom Gland.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu H., Xiang K., Wang Y., Liu J.;
"A chain of ACF 1/2 from Deinagkistrodon acutus.";
"A chain of ACF 1/2 from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY091758, AAM22786.1;
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PR0059; lectin_c: 1.
PRINTS; PR01504; PUCKEAIITSAP.
SMART; SM00034; CLECT: 1.
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PROSITE; PSS0041; C TYPE LECTIN 2; 1.
SEQUENCE 152 AA; 17108 MW; B0870F3DAOA4D23B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   5C59C0F503A4D223 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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89.7%; Pred. No. 2e-14;
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Pfam; PF00059; lectin c; 1.
PROMOTT; SMO0034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
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                                                                                    Anticoagulant protein A precursor.
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152 AA; 17124 MW;
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Wang W.-J., Ling Q.-D., Huang T.-F.;
"Molecular structure and functional characterization of agglucetin, a
"tetrameric glycoprotein Ib-binding protein, from Formosan pit viper.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS40647; AAN23126.1;
                                                                                                                                                                                                                                SECURNCE FROM N.A.
MEDLINE=21542539; PubMed=11686327;
Wang W.J., Huang T.F.;
"A novel terrang round protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist.";
Thromb. Haemost. 86:1077-1086(2001).
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Agkisacutacin B chain.
Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                   Edutaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Agglucetin-beta 1 subunit precursor.
Agkistrodon acutus (Hundred-pace snake)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF776421; AAF26287.1; -
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2342BAE38EBOCCB9 CRC64;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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1; Mismatches
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146 AA
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InterPro; IPR003990; Pancreatis_ac.
Pfam; PR0059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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24 146 A
146 AA; 16728 MW;
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PRELIMINARY;
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Matches 24; Conserv
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Query Match
Best Local Similarity 72.4<sup>5</sup>
Matches 21, Conservative
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SEQUENCE FROM N.A.
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ACF 1/2 B-chain.
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01-JUN-2001
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Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.;
"The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom.";
Thromb. Haemost. 79:1199-1207(1998).
ENBL: AB019616; BA34425.1; -.
HISSP: P23807; IIXX.
InterPro; IPRO1304; Lectin_C.
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
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                                                                                       80.0%; Score 136; DB 13; Length 146; 75.9%; Pred. No. 1e-11;
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SMART; SM00034; CLECT; 1.7

PROSITE; PS00615; C TYPE LECTIN 1; 1.7

PROSITE; PS50041; C TYPE LECTIN 2; 1.7

SROHENCE 146 AA; 17064 MW; PEDA84BDCC24E76D CRC64;
PS00615; C_TYPE_LECTIN 1; 1.
PS50041; C_TYPE_LECTIN 2; 1.
146 AA; 16726 MW; 7360B6D6864131BB_CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anticoagulant protein-B precursor.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=61300;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Deinagkistrodon.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Deinagkistrodon.
anticoagulant protein from Deinagristrodon actus venom gland."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB036801; BAB20441.1; --
HSSP; P23807; IIXX.
HSSP; P23807; IIXX.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PP00059; Jectin C; 1.
Pfam; PR0059; PROTEATITSAP.
SWART; SM00034; CLECT; 1.
PROSITE; PS00061; C_TYPE_LECTIN 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tu H., Xiang K., Wang Y., Liu J.;
"B chain of ACF 1/2 from Deinagkistrodon acutus.";
"Butitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AXO91761, AAM22789.1;
InterPro; IPR001304; Lectin C.
InterPro; IPR009990; pancreatis_ac.
Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                      SIGNAL 1 23 POTENTIAL.
SEQUENCE 146 AA; 16997 MW; 420D71EBE4E9F5D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
SEQUENCE 146 AA; 16925 MW; F2493CACBASD2144 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 133; DB 13;
Pred. No. 2.7e-11;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                      th 78.2%; Score 133; DB 13; L Similarity 72.4%; Pred. No. 2.7e-11; 21; Conservative 2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 DCPSDWSSYEGHCYKPFNEPKNWADAENF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aggretin beta chain (Fragment)
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Rukaryota; Merazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Venom gland;
MEDLINE=9944311; PubMed=10512747;
C.H., Au L.C., Huang T.F.;
"Molecular cloning and sequence analysis of aggretin, a collagen-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%; Score 124; DB 13; Length 146; 69.0%; Pred. No. 5.2e-10; ive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.7%; Score 127; DB 13; Length 146; 69.0%; Pred. No. 1.9e-10;
                                                                                            Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H., "A Novel Coagulation Factor Xa Inhibitor from Korean Snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Venow gland;
Chung C.H., Au L.C., Huang T.F.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF244901; AAF79953.1; -.
HSSPP, P23807; IIXX.
InterPro; IPR001304; Lectin C.
InterPro; IPR0013990; Pancreatis_ac.
                                                                                                                                     (Agkistrodon halys) venom.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF197915; AAG28522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          24 146 HALYXIN B-CHAIN.
146 AA; 16841 MW; C47D8A43B0A00709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER 146 146 - SEQÜENCE 146 AA; 16770 MW; 930839140CFD8908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          platelet aggregation inducer.";
Biochem. Biophys. Res. Commun. 263:723-727(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; Process; lecting; 1.
PRINTS; PRO1504; PRCEATITSAP.
SMART; SMO0034; CLECT; LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                             PROSITE, PS00615, C TYPE LECTIN 1, 1. PROSITE, PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                              InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 69.0
ses 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                              HSSP; P23807; 11XX
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                  NCBI_TaxID=8714;
                                                                                                                                                                                                                                                                                                                                                                              24.
                                                                                 rissum=Venom
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     Signal.
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Matches
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01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Halyxin B-chain precursor.
Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pallas).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
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                                                                                                                                                                                                                                                                                            77.6%; Score 132; DB 13; Length 124; 72.4%; Pred. No. 3.1e-11; ive 2; Mismatches 6; Indels 0
                                  SEQUENCE FROM N.A.

TISSUE-Venom gland;
ZISSUE-Venom gland;
ZUA X., Xu X.;
Submitted (RE.,
Submitted (RE.,
Submitted (RE.,
RSP);
RSP);
PS3807; 11XX.
HSSP; PS3807; 11XX.
HSSP; PF800159; Lectin_C.
Ffam; PF00059; Lectin_C;
PFam; PF00059; CLECT; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE LECTIN_1; 1.
PROSITE; PS00615; C_TYPE LECTIN_2; 1.
SEQUENCE 124 AA; 1470I MW; 46B2D5B0CB3DC518 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu H., Xiang K., Wang Y., Liu J.;
"B chain of agkisacutedin from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY091756; AAM22785.1;
                                                                                                    the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0615; C_TYPE_LECTIN 1; 1.
PROSITE; PSS0041; C_TYPE_LECTIN 2; 1.
SEQUENCE 146 AA; 16740 MW; 6260B6D68741317C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                            1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29
                                                                                                                                                                                                                                                                                                                                                                                                           DCPSDWSSYEGHCYKPFNELKNWADAENF 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                     Local Similarity 72.4%;
les 21; Conservative
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hes 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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    NCBI_TaxID=36307;
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Q9DG31
D Q9DG3
AC Q9DG3
DT 01-MA
DT 01-MA
DE HAllyx
OS Agkis
OS Agkis
OS Bukat
OC Ebukat
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1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF

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C-type lectin.
Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAY-2003 (TEMBLrel. 23, Last annotation update)
01-MAY-2003 (TEMBLrel. 23, Last annotation update)
ECLV IX/X-BP alpha SUBUNIT-COAGULATION factor IX/factor X-binding protein alpha subunit.
Echis carinatus (Saw scaled viper).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Lepidosauria, Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae, Viperinae; Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Y.L., Tsai I.H.; "Function of coagulation factor "Functional and sequence characterization of coagulation factor IX/factor X-binding protein from the venom of Echis carinatus
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Yu H., Xiang K., Wang Y., Liu J.;

Yu H., Xiang K., Wang Y., Liu J.;

"Member of C-type lectin family from Deinagkistrodon acutus.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY091760; AAM22788.1; -..

InterPro; IPR001304; Lectin. C.

InterPro; IPR003990; Pancreatis.ac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 155 AA; 17944 MW; 3E935FF53773AB94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR01334; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM0034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
SEQUENCE 131 AA; 15439 MW; B05E6C5CBF317E24 CRC64;
                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                               155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA.
24 DCPSGWSSYEGHCYKPFNEPKNWADAERF 52
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                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 35:5264-5271(1996)
HSSP; P23806; 11XX.
                                                                                            PRELIMINARY;
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Matches
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Q9PSM9
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Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshimaru M., Chijiwa T., Chang C., Fukumaki Y., Ohno M.;
"Characterization and molecular evolution of an anticoagulant protein
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Ingpidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea; Viperidae, Crotalinae, Trimeresurus.
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0
                    Length 131;
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                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Agkistrodon actus venom.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO46491; BAB21452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PROISO, PNCREATITAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS0041; C_TYPE_LECTIN 2; 1.
SEQUENCE 146 AA; 16461 MW; 6ADF0B032544316C CRC64;
                                                                                                                                                                                                                01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Factor XI/factor X binding protein A chain.
                 72.4%; Score 123; DB 13; 69.0%; Pred. No. 6.4e-10; ive 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.4%; Score 123; DB 13; 74.1%; Pred. No. 7.2e-10; iive 2; Mismatches 5;
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                                                                                               1 DCLPGWSSHEGHCYKVFNEYKTWKDAEKF
                                                                             1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF
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                                                                                                                                                                                        PRT;
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InterPro, IPR003990, Pancreatis ac.
Pfam, PF00059, lectin c, 1.
                                                                                                                                                                                                                                                                                                 Trimeresurus flavoviridis (Habu)
Query Match
Best Local Similarity 69.0%,
...ea 20, Conservative
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Matches 20; Conservative
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us-09-938-114-3.rst

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

December 8, 2003, 13:34:19; Search time 751.514 Seconds (without alignments) 937.879 Million cell updates/sec Run on:

US-09-938-114-3

170 1 DCSSDWSSYEGHCYKVFKQSKTWTDAESF 29 Perfect score: Sequence:

BLOSUM62 Scoring table:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Command line parameters:

EST:* Database :

em_estin: *
gb_esti: *
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em gss hum: *

em_gss_inv:* em_gss_pln:* em gss vrt:* mam: * em gss

em gss mus: *
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em gss phg: *
em gss vrl: *

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ion	1696 PH1A01F	401618 JT.1C07F	01469 JH1E0	01621 JL1D02F	01628 JL1E12F	01667 JL2H07F	01495 JH2B09F	01656 JL2E04F	01686 PH015FB	01620 JL1C11F	BM401417 GH061F Sn BM401401 CH005FF Sn	01654 JT.2007E	01460 JH1D06	01520 JH2G02F	552 JH3E12F	01598 JH4F11F	682	01669 JL2H0	99404	55510	38882 60295521	00634 60413767	0042 6034	10105 60315865	9519 603159	65 60348773	7176 60311504	97747 HOA25-1-	04 HOA25-1-	11081 HOA53-1	50485 7a27b11.	19799 HOA40-1	94039 Dan	29062 HNC1	07207 RC-BT1	25582 HNC30-1-	29205 HNC59-1	209 60281187	23232 603490	66055 60381532	69611 60	30613 60339965	60029 60347625
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ALIGNMENTS

LOCUS RESULT 1 BM401696

BM401696 172 bp mRNA linear EST 01-MAY-2002 PH1A01F Snake Bothrops insularis library IL2 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence. BM401696.1 GI:20376324 EST. BM401696

Bothrops insularis (island jararaca) Bothrops insularis ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

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/mol_type="mrxn"
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//tissue type="venon glands"
//tissue type="venon glands, vector; pGEMILET; site_1: Econome glands, vector; pGEMILET; site_1: Econome glands, vector; pGEMILET; site_1: Econome glands were primed with oligo-(dT) and reverse risals and cloning with oligo-(dT) and reverse venome glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscribe Plasmid System for cDNA synthesis and cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILET + vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
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391 bp mRNA linear EST 01-MAY-2002
JH1E09F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
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A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                    Contact: Paulo Lee Ho
Contro de Biotecnologia
Instituto Butanta 1500, Sao Paulo SP, BRAZIL, 05503-900
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 1505
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITLOIA (see Reference)
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of
                              Junqueira-de-Azevedo, I.L.M. and Ho.P.L.
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Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                    Contact: Paulo Lee Ho
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Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                    Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
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/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Organ: venom glands; Vector: pSEMIJEIF; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMIJEF+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putarive identification of each EST of
cluster was obtained through Blast searches (e-value <
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JL1D02F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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1 (bases 1 to 475)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
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the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                   Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL03A (see Reference)
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Matches:
Conservative:
Mismatches:
Indels:
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Bothrops insularis
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                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:8723"
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                                         Contact: Paulo Lee Ho
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/mol type="memba"
//mol type="memba"
//mol type="memba"
//db_xref="taxon:8723"
//tisaue type="venom glands"
//clone lib="soans glands"
//clone lib="soans glands"
//clone lib="soans glands"
//note="Organ: venom glands; Vector: pGEM11Zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM12f+ vector (Promega). ESTs were generated from random clones and grouped in unique
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 504)
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A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
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22347338
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/tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, vector: pGEMIIZE+; Site_I: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to CDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The CDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMIIZE+ vector (Promega). ESTS were generated from random clones and grouped in unique sequences. The putarive identification of each EST or cluster was obtained through Blast searches (e-value <
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1 (Dases 1 to 512)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butanta.
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 1505
Fax: 55 11 37 26 1505
Email: hopleequep.br
This EST corresponds to cluster BITLOIA (see Reference)
This EST corresponds to cluster BITL01A (see Reference)
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Bothrops insularis
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/db_xref="taxon:8723"
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// Ab xref="taxon:8723"
/ Ab xref="taxon:8723"
/ Lisue type="wenom glands"
/ Clone lib="snake Bothrops insularis library IL3"
/ Clone lib="snake Bothrops insularis library IL3"
/ Clone lib="snake Bothrops insularis bothrops insularis rooth representation of the library IL3"
/ Clone lib="snake Bothrops insularis bothrop in slands were primed with oligo-(dT) and reverse riands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarces gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGBM112f+ vector (Promega). ESTS were generated from random clones and grouped in unique sequences. The putative identification of each EST of the putative id
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1 (bases 1 to 510)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.

A survey of gene expression and diversity in the venom glands of expressed sequence tags (ESTB)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
  Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hople@usp.br
This EST corresponds to cluster BITL01A (see Reference)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Bothrops insularis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hoplee@usp.br
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78.57%
71.43%
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Best Local Similarity:
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TITLE
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Contact: Paulo Lee Ho
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76.92%
73.08%
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Best Local Similarity:
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12459276
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DB:
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TITLE
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                                BM401656 343 bp mRNA linear BST 01-MAY-2002 JL2E04F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5, similar to Snake venom C-type lectin, mRNA sequence.
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1 (bases 1 to 343)

Unqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Paulo Lee Ho
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL01A (see Reference)
                                                                                                                                                                                                                                           5 others
                                                                                                                                                                                                                                                                                               512
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Matches:
Conservative:
Mismatches:
Indels:
           'organism="Bothrops insularis"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bothrops insularis (island jararaca)
Bothrops insularis
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Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 LysThrTrpThrAspAlaGluSer 28
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                          /mol_type="mRNA"
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BM401656.1 GI:20376284
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71.43%
74.71%
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Best Local Similarity:
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VERSION
KEYWORDS
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AUTHORS
TITLE
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MEDLINE
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/db_xref="taxon:8723"
/tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops; Vector: pGEM11Z±+; Site 1: Bco
R15 Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11Zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putarive identification of each EST or
cluster was obtained through Blast searches (e-value <
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1 (bases 1 to 633)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

601.2), 279-291 (2002)
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/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
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Instituto Butantan
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
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Matches:
Conservative:
Mismatches:
Indels:
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Bothrops insularis (island jararaca)
Bothrops insularis
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BM401686.1 GI:20376314
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Tue Dec

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/mol type="mRNA"
/db_xref="taxon:8723"
/db_xref="taxon:8723"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, Vector: pGEM11Zf+; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
/note="Organ: venom glands; Vector: pGEM11Zf+; Site_1: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to CDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The CDNAs were selected by Size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11Zf+ vector (Promega). ESTs sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
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JLIC11F Snake Bothrops insularis library IL3 Bothrops insularis
CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GATTGTCCCTCTGATTGGTCCCCCTATGGAGGCATTGCTACAAGCTCTTCAAACAACGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

Viperidae; Crotalinae; Bothrops.

J. (bases 1 to 378)

J. unqueira-de-Azevedo, L.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hoplee@usp.br
This EST corresponds to cluster BITL11A (see Reference)
                                                                                                                                                                                                                                                                                            14 others
                                                                                                                                                                                                                                                                                                                                                                                      633
119
7
0
                                                                                                                                                                                                                                                                                                                                                                                    Length:
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Conservative:
Mismatches:
Indels:
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paul
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 ATGAACTGGGCGGATGCAGAGAAT 165
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67.86$
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BM401620
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transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGBM11Zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
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GH061F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5. similar to Snake venom C-type lectin, mRNA sequence.
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// db xref="texcn:8723"
// tissue type="texcn:8723"
// tissue type="texcn:8723"
// clone lib="snake Bothrops insularis library IL2"
// clone lib="snake Bothrops insularis streets in Ec. Mote="Organ: venom glands, Vector: pGEMILZf+; Site_1: Ec. RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in
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1 (bases 1 to 574)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
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Matches:
Conservative:
Mismatches:
Indels:
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Bothrops insularis
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BM401417.1 GI:20376045
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Best Local Similarity:
Query Match:
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/clone_lib="Snake Bothrops insularis library IL2"
/clone_lib="Snake Bothrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEM11Zf; Site_1: Eco
/note="Organ: venom glands; Vector pGEM11Zf; Site_1: Eco
/note="Organ: venom glands; Vector pGEM11Zf; Site_1: Eco
/note State_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Sytthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (150-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11Zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM112f+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
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GH025F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5' similar to Snake venom C-type lectin, mRNA sequence.
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1 (bases 1 to 654)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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                                                                                                                       4 others
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/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
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Bothrops insularis
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Gene 299 (1-2), 279-291 (2002)
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BM401401.1 GI:20376029
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                                                                                                                     129 c
                                                                                                    e-05)."
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/mol type="mRNA"

/db xref="taxon:8723"

/db xref="taxon:8723"

/tissue type="venom glands"

/clone lib="Snake Bothrops insularis library IL3"

/clone lib="Organ: venom glands; Vector: pGEMILZf+; Site l: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo- (dr) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gelelelectrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZf+ vector (Promega). ESTS were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
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1 (bases 1 to 301)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)
     sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
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JL2D07F Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Contact: Paulo Lee Ho
Contact e Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL14A (see Reference)
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/organism="Bothrops insularis"
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Matches:
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Bothrops insularis
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BM401520
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AUTHORS
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/clone_library library libra
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JHIDO6F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5, similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Uperidae, Crotalinae, Bothrops.

1 (Dases 1 to 460)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL13A (see Reference)
Seg primer: M13F.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                    Alignment Scores:
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     SASE COUNT
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
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A survey of gene expression and diversity in the venom glands of
the piruiper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
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Mismatches:
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Bothrops insularis
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Conservative: 2
Mismatches: 7
Indels: 0
Gaps: 0
                                                       US-09-938-114-3 (1-29) x BM401520 (1-374)
   74.07%
66.67%
65.88%
12
Percent Similarity:
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Query Match:
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Op δ qq

²¹ LysThrTrpThrAspalaGlu 27 190 TTGAAGTGGGAGGATGCAGAG 210

Search completed: December 8, 2003, 17:24:33 Job time: 754.514 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2003, 09:45:44 ; Search time 10.2 Seconds (without alignments) 264.544 Million cell updates/sec 8 December Run on:

US-09-938-114-4

Perfect score:

1 DCPSEWSSYEGFCYKPF 17 Sequence:

BLOSUM62 Scoring table:

1107863 seqs, 158726573 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

		Description	Deinagkistrodon ac	Ahvlysantinfarotas	Snake venom blood	Stake were book	Snake wenom derive	N-retminal segment	Semience of the ri	Segment of polyme	Vipera palestinae	
	Ţ.	77	ABU08799	ABB83143	AAM51540	AAM51544	AAR71980	AAR23886	AAR24427	AAR38225	AAR72232	
	2	3	24	23	22	22	16	13	13	14	16	
	Query	110000	146	120	30	146	21	28	116	123	30	
ķo	Query		93.5	88.0	87.0	87.0	79.6	79.6	79.6	79.6	77.8	
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AAR72231	AAR722		AAR7223	,	AAR7223		•		·	AAR7197		AA020973		AA020981			AA02098		AA02098		AA020988	AA020989	AA020990	AA020991	AA020992	AA020993	AA020994	AA020995	AA020996	AA020997	AA020998	AA020999	AAR24426	AAR71981	AAY85628
16	16	13	16	16	16	23	13	16	23	16	21	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23			23		16	21
32	43		52	127	132	145	36	38	110	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	127	149	149
77.8	77.8	77.8	77.8	77.8	77.8	77.8	76.9	76.9	٠		Ġ	ė.	6.92	9	9	9	76.9	9	76.9				76.9		76.9			9	ė.	ġ.	9	9	6.97	6.94	76.9
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ALIGNMENTS

ABU08799 standard; Protein; 146 AA. (first entry) 02-JUN-2003 ABU08799; RESULT 1 ABU08799

Deinagkistrodon acutus antithrombosis enzyme beta chain.

Antithrombosis, beta chain, fibrin hydrolysis, blood clot, enzyme; platelet aggregation; vaso-occulusive disorder, thromboembolic disorder; myocardial infarction; restenosis, cancer; neurodegenerative disease; angiopathic thrombosis; cerebral thrombosis; thromboanjitis obliterans; ischaemic cerebral vascular disease, unstable angina; acute thrombosis; unstable stenocardia; pulmonary embolism, deep vein thrombosis; oedema; peripheral arterial occulsion; stroke; atherosclerosis; inflammation; thrombosis

Deinagkistrodon acutus.

'note= "Leader peptide" Location/Qualifiers Peptide Protein

24..146 /note= "Mature antithrombosis enzyme beta chain. Residues 24 to 40 specifically claimed in claim 8" /label= Unknown Misc-difference 72

/note= "Encoded by TNN" /label= Unknown Misc-difference

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chromatographic process to separate and purify and the repurifying the thrombase in a fast protein purifying work station. It was found that the Ahylysantinfarctase thrombase II consists of two subunits, Subunit A (ABB83142) and Subunit B (the present sequence).
                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for purifying Ahylysantinfarctase thrombase II from the snake venom of Chinese Agkistrodon acutus. The method involves using an anionic exchange column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halyxin as blood anticoagulation protein separated from snake venom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.0%; Score 95; DB 23; Length 120; 82.4%; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                              Ahylysantinfarctase thrombase and its production process
                                                                                                                                                                           (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 5 (Disclosure); 8pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                29-APR-2001; 2001CN-0115570.
                                                                                                                                       29-APR-2001; 2001CN-0115570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOB-) BIOBUD CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-637330/73
                                                                                                                                                                                                                                                          WPI; 2002-281833/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jung GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agkistrodon halys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KR2001049671-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-1999;
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                CN1332242-A
                                                        23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM51540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jang YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                       Xiao C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
AAM51540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3est
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition is useful for preventing and treating vaso-occuluaive and thromboembolic disorders, including myocardial infarction, restenosis, angiopathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thrombosangiitis obliterans, pulmonary embolism, deep vein thrombosis, peripheral arterial occulsion, stroke. It is also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral arterial occulsion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents the amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.005 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              purified Agkistrodon actus anti-thrombosis enzyme, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.5%; Score 101; DB 24; Length 146; 94.1%; Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ahylysantinfarctase thrombase II subunit B; snake; venom;
Chinese Agkistrodon acutus; purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinagkistrodon acutus antithrombosis enzyme beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ahylysantinfarctase thrombase II subunit B.
                                                                                                                                                                                                                                                                                                                           (HEFE-) HEFEI SIU FUNG USTC PHARM CO LTD.
  /note= "Encoded by NNN"
                                                                                                                       by NNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1; 19pp, English.
                                                            'note= "Encoded
                                                                                                                    /note= "Encoded
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0
                                         Unknown
                                                                                                    /label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCPSEWSSYEGHCYKPF 40
                                                                                                                                                                                                                                              98US-0058740.
                                                                                                                                                                                                                                                                                   97US-043886P
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                                         /label=
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-352116/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agkistrodon acutus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AA;
                                                                                                                                                                                                                                                                                                                                                              Cheng X;
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABX93674
                      Misc-difference
                                                                                 Misc-difference
                                                                                                                                                                                                                                              10-APR-1998;
                                                                                                                                                                                                                                                                                   10-APR-1997;
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Gaps

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Indels

Son

ABB83143;

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RESULT 2 ABB83143

Sequence

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can
be used in the treatment of thrombogenesis. The present sequence is
a peptide derived from the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                          Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%; Score 94; DB 22; Length 146;
88.2%; Pred. No. 2e-05;
iive 0; Mismatches 2; Indels
                                                                           87.0%; Score 94; DB 22; Length 30;
88.2%; Pred. No. 4.9e-06;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                 Snake venom blood anticoagulant halyxin B chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Son YD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koo BH,
                                                                                                                                                                                                                        AAM51544 standard; Protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 11-12; 21pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR71980 standard; peptide; 21 AA.
                                                                                                                                17
                                                                                                                                                       1 DCPSGWSSYEGHCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DCPSGWSSYEGHCYKPF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2000; 2000KR-0036591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99KR-0025105
                                                                                                                               1 DCPSEWSSYEGFCYKPF
                                                              Query Match
Best Local Similarity 88...
Best Local 15; Conservative
                                                                                                                                                                                                                                                                        (first entry)
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hes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jung GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 AA;
                                                                                                                                                                                                                                                                                                                                                                  Agkistrodon halys
                                                    30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAI71877
                                                                                                                                                                                                                                                                                                                                                                                          KR2001049671-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1999;
                                                                                                                                                                                                                                                                        10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2001
                                                                                                                                                                                                                                                                                                                                         thrombosis.
                                                                                                                                                                                                                                                AAM51544;
                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jang YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR71980;
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Matches
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AAR71980
ID AAR7
XX
AC AAR7
XX
DT 25-M
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                                                                                                                                                                                                                                                                                                                                                                                    AAR71980 is a snake venom derived antithrombotic peptide, prepared by cleaving the interpeptide but retaining the intrapeptide disulphide bonds of the original snake venom oligopeptide. The peptide has the advantage of avoiding significant thrombocytopenia when administered at the minimum dose, for in vivo inhibition of platelet von Willebrand factor binding.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal sequence of the earlier eluting subunit (CHH-B-beta) of the later eluting peak of the platelet antiadhesive peptide (PAA).
                                                 Antithrombotic peptide, snake venom; platelet binding inhibition; von Willebrand factors; Crotalus horridus horridus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                           oligopeptide from snake venom to break inter-chain disulphide bonds but preserve intra-chain disulphide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.6%; Score 86; DB 16; Length 21; 76.5%; Pred. No. 4.4e-05; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                Nagano M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Platelet adherence inhibitor; platelet anti-adhesive;
antithrombotic agent; von Willebrand Factor;
platelet glycoprotein GPIb-IX complex.
                                                                                                                                                                                                                                                Kobayashi T,
                        Snake venom derived antithrombotic peptide.
                                                                                                                                                                                                                                               Kito M, Kobay,
Yoshimoto R;
                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 45; 84pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR23886 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
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                                                                                                                                                                     94WO-JP01555
                                                                                                                                                                                            93JP-0236975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91WO-US08516.
                                                                                        Crotalus horridus horridus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DCPSEWSSYEGFCYKPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DCPSDWSSYEGHCYRVF
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 76.5
les 13; Conservative
                                                                                                                                                                                                                                           Fukuchi N, Ishii K, K
Tanaka A, Yamamoto H,
                                                                                                                                                                                                                    (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                   WPI; 1995-139559/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AA;
                                                                                                                                                                 21-SEP-1994;
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                                                                                                                                                                                            22-SEP-1993;
28-NOV-1995
                                                                                                               WO9508573-A1
                                                                                                                                          30-MAR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 kDa and about 15 kDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of AAR38224 has been found, characterised by Asp at posn. three in lieu
      The PAA was purified from a solution of snake venom. Analysis of the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with a mol. wt. 23-28 kD. Both were able to inhibit botrocetin and ristocetin induced platelet agglutination. They were alled CHH-A and CHH-B. The earlier aluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-alpha) were individually submitted to V-terminal sequence analysis. The complete amino acid sequence (Ordated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                        79.6%; Score 86; DB 13; Length 116; 76.5%; Pred. No. 0.00021; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.6%; Score 86; DB 14; Length 123; 76.5%; Pred. No. 0.00022; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New platelet-binding proteins obtained from snake venom -
binding of von Willebrand factor to platelet membrane
glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of polypeptide chain of alboaggregin A (AL-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venom; snake; platelet-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR38225 standard; protein; 123 AA.
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92US-0893929.
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                                                                                                                                                                                                                                                                                                                                             1 DCPSEWSSYEGFCYKPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76...
Conservative
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trimeresurus albolabris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-196991/24.
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Matches 13: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA;
                                                                                                                                                                                                                       116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09311151-A1
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01-OCT-1993
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                                                                                                                                                                                                                                                                                                   The PAA was purified from a solution of snake venom. Analysis of the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with a mol. wt. 23-28 kD. Both were able to inhibit, botroocetin and ristocetin induced platelet agglutination. They were called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-beta) to N. terminal sequence analysis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of the platelet glycoprotein GPIb inhibitor beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit thrombus formation; for treatment of arteriosclerosis, atherosclerosis, acute myocardial infarction, chronic unstable
                                                                                                                                                            Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit thrombus formation; for treatment of arteriosclerosis, atherosclerosis, acute myocardial infarction, chronic unstable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Platelet adherence inhibitor; platelet anti-adhesive; antithrombotic agent; von Willebrand Factor; platelet glycoprotein GPIb-IX complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR24427 standard; Protein; 116 AA
                                                                                                                                                                                                                                                                 Claim 4; Page 30; 5pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCPSEWSSYEGFCYKPF 17
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                                        (CORT-) COR THERAPEUTICS INC
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    90US-0614443.
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(first entry)
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                                                                                                                        WPI; 1992-199936/24.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 AA;
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                                                                                Scarborough RM;
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    16-NOV-1990;
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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Vipera palestinae, venom, N-terminal fragment, antithrombotic agent, platelet binding, von Willebrand factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                      AAR72232 standard; peptide; 30 AA.
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                             1 DCPSDWSSYEGHCYRVF 17
DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0241666.
94JP-0002691.
94JP-0128518.
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(first entry)
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Best Local Similarity 76.5'
Matches 13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-147392/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vipera palestinae.
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14-JAN-1994;
10-JUN-1994;
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04-DEC-1995
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                                                                                                                                                                                                                                                 AAR72232;
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AC AAR7
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DT 25-V
DT 04-I
DT 04-I
DX VIPE
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VIPE
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AAR72231 is a Vipera palestinae venom derived N-terminal fragment, the full peptide is given in AAR72235. A peptide compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti-
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                          Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
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                                                                                                                                                                                                                                                                                                                                         thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                 Kobayashi
platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR72234 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                      Claim 3; Page 17; 37pp; Japanese.
                                                                                                                                                                                 Fukuchi N, Ishii K, Kaida K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DCPSEWSSYEGFCYKPF 17
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94JP-0002691.
94JP-0128518.
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(first entry)
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                                                                                                                                                         (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                      WPI; 1995-147392/19.
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                      Vipera palestinae
                                                                                                                                                                                                                                                                                                                                                                           32 AA;
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                                                                                       27-SEP-1994;
                                                                                                                         14-JAN-1994;
                                           WO9509183-A1
                                                                                                             28-SEP-1993;
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10-JUN-1994;
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04-DEC-1995
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Kobayashi T;

Fukuchi N, Ishii K, Kaida K,

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50 AA;

Sequence

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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The PAA was purified from a solution of snake venom. The earlier eluting subunit, PP-beta was subjected to Edman degradation for 50 cyles to obtain the sequence in AAR23889. The later eluting sequence - the PP-alpha chain was determined for 31 cycles to give the SQ in AAR23890.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal sequence of the earlier eluting subunit PP-beta of the later eluting peak of the platelet antiadhesive peptide (PAA)
                                        ptide derived from Vipera palestinae venom - inhibits binding platelets to von Willebrand factor, useful as antithrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit thrombus formation; for treatment of arteriosclerosis, atherosclerosis, acute myocardial infarction, chronic unstable
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                                                                                                                                                                                                                                                                   77.8%; Score 84; DB 16; Length 43;
.larity 76.5%; Pred. No. 0.00016;
Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Platelet adherence inhibitor; platelet anti-adhesive; antithrombotic agent; von Willebrand Factor; platelet glycoprotein GPIb-IX complex.
                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR23889 standard; Protein; 50 AA.
                                                                                                       Claim 4; Page 18; 37pp; Japanese.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudocerastes persicus.
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                 WPI; 1995-147392/19.
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                          43 AA;
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21-NOV-1992
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                                            Peptide
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                        Gaps
                                                                                                                                                                                                                                       Vipera palestinae, venom, N-terminal fragment, antithrombotic agent, platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
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                                                                                                                                                                                                                  Vipera palestinae venom derived peptide N-terminal fragment
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77.8%; Score 84; DB 13; Length 50; 76.5%; Pred. No. 0.00018;
                      2; Indels
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                        2; Mismatches
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                                                                                                                                  AAR72233 standard; peptide; 52 AA.
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                                                1 DCPSEWSSYEGFCYKPF 17
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(first entry)
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hes 13; Conservative
Query Match
Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           (AJIN ) AJINOMOTO KK
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                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1994;
                                                                                                                                                                                25-MAR-2003
04-DEC-1995
                                                                                                                                                                                                                                                                                                                              06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukuchi N,
                                                                                                                                                          AAR72233;
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10-JUN-1994;
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                                                                                                                                                                                                                                                                                              AAR72236 is a Vipera palestinae venom derived peptide. A peptide compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti-thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                          Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 84; DB 16; Length 127; 76.5%; Pred. No. 0.00043; Live 2; Mismatches 2; Indels
                                            Vipera palestinae; venom; antithrombotic agent; platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vipera palestinae; venom; antithrombotic agent; platelet binding; von Willebrand factor.
                                                                                                                                                                                                       Kobayashi T;
                            Vipera palestinae venom derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vipera palestinae venom derived peptide.
                                                                                                                                                                                                                                                                            Claim 5; Pages 19-20; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR72235 standard; peptide; 132 AA.
                                                                                                                                                                                                       Kaida K,
                                                                                                                                                                                                                                                                                                                                                                                                              1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                               93JP-0241666.
94JP-0002691.
94JP-0128518.
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94JP-0002691.
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(updated)
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(first entry)
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                                                                                                                                                                                    (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                      Fukuchi N, Ishii K,
                                                                                                                                                                                                                        WPI; 1995-147392/19.
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                       127 AA;
                                                                        Vipera palestinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vipera palestinae
                                                                                          WO9509183-A1.
                                                                                                                            27-SEP-1994;
                                                                                                                                                28-SEP-1993;
                                                                                                                                                         14-JAN-1994;
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14-JAN-1994;
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25-MAR-2003
04-DEC-1995
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04-DEC-1995
                                                                                                            06-APR-1995
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Matches
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AAR72235 is a Vipera palestinae venom derived peptide. A peptide compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti-thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 84; DB 16; Length 132; 76.5%; Pred. No. 0.00044; Live 2; Mismatches 2; Indels
                                                                                                 H
                                                                                                    Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: December 8, 2003, 09:52:34 Job time: 10.2 secs
                                                                                                                                                                                                                                                                                                     Claim 5; Page 19; 37pp; Japanese.
                                                                                                 Kaida K,
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94JP-0128518.
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Best Local Similarity 76.5
Matches 13; Conservative
                                               (AJIN ) AJINOMOTO KK.
                                                                                                 Fukuchi N, Ishii K,
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                                                                                    December 8, 2003, 09:50:40; Search time 3.69143 Seconds (without alignments) 194.853 Million cell updates/sec
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Sequence 5,
Sequence 5,
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-612-840A-3
US-07-614-443A-2
US-08-294-859-2
US-08-481-676-2
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US-08-612-840A-2
US-07-614-443A-1
US-08-294-859-1
US-08-481-676-1
US-08-612-840A-8
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PCT-US92-10344-3
US-07-893-929A-7
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US-09-058-740-2
US-07-893-929A-6
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PCT-US92-10344-4
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US-07-893-929A-8
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US-08-481-676-5
                                                                                                                                                                                                                                               328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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ALIGNMENTS

US-09-058-740-4

Sequence 4, Application US/09058740

Patent No. 6489411

GENERAL INFORMATION

Jun-Guo Ding, Hau, Wan-Zhi Hanag,
Zhen-Yu Xu, Dan Luo, Lian-Di Kanag,
Zhen-Yu Xu, Dan Luo, Lian-Di Kanag,
Zhen-Yu Xu, Dan Luo, Lian-Di Kanag,
Jin-Guo Ding, Fang Rong, Yan Liu and
Hui-Ran Chen WIND FROM ANTITHROMBOSIS ENZYME FROM THE SNAKE

UNDMER OF ENDURINGES 12

CORRESPEEL LYON & LYON

STREET: 633 West Fifth Street

CITY: Los Angeles

STREET: 633 West Fifth Street

CITY: Los Angeles

COMPUTR: T. 0.5.A.

ZIP SOUT-2066

COMPUTR: READABLE FORM:
MEDIUM TYPE: 3.5.P DISKETCE, 1.44 Mb

COMPUTR: READABLE FORM:
MEDIUM TYPE: 3.5.A.

ZHORESPEEL CANATON

COMPUTR: READABLE FORM:
MEDIUM TYPE: 3.5.A.

SOUTHARR: PAPELCATION NUMBER: v0/09/058,740

FILING DATE: 10-APT-1999

CLASSIFICATION NUMBER: v0/06/058,740

FILING DATE: 10-APT-180

CLASSIFICATION NUMBER: 38,673

REGISTRACTON NUMBER: 23,298

TELEROWE: CHAN, Anthony

REGISTRACE CHANCTENTION SUMBER: 38,673

TELEROWE: CHANCTENTION SEQ ID NO: 4:

SEQUENCE CHANCTENTION: SEQ ID NO: 4:

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND TITLE OF INVENTION: METHOD OF PRODUCING THE SAME NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
                                  100.0%; Score 108; DB 4; Length 17; 100.0%; Pred. No. 3.8e-09; Live 0; Mismatches 0; Indels
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1 Similarity 76.5%; Pred. No. 6e-06;
13; Conservative 2; Mismatchee
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION TO ATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 22-SEP-1993
ATTONNEY/AGENT INFORMATION:
NAME: NO. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-614-443A-2; Sequence 2, Application US/07614443A; Patent No. 5342830
                                                                                                                                                                                                                                             Sequence 3, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
                                                                                                                                                                                                                                                                                                       FUKUCHI, Naoyuki
XAMANOTO, Hiroshi
NAGANO, Mitsuyo
KITO, Morikazu
TANAKA, Akiko
ISHII, Koichi
KOBAYASHI, Tsuyoshi
YOSHIMOTO, Ryota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
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                              Ouery Match
Best Local Similarity 100.
Matches 17, Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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STATE: VA
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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  US-09-058-740-4
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                                                                 GENERAL INCOMMATION:
APPLICANT: SCAREGOROUGH, ROBERT M.
APPLICANT: SCAREGOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster
STREET: 2000 Fennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
CUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BRACCOMPATIBLE
COMPUTER: BAPENCATION AGENTIAL Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
CLASSIFICATION: 435
APPLICANT: SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:
                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSE: MOTIFICAD & POETEER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-294-859-2
; Sequence 2, Application US/08294859
; Patent No. 5679542
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SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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Best Local Similarity 76.5
Matches 13; Conservative
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Sequence 4, Application US/07893929A
                                      Patent No. 5336667
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                                                                                                                                                                                                                                    Length 117;
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MEDLUM TYPE: Floppy disk
COMPUTER: Flam P.C.DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/481,676
FILING DATE: 07-JUN-1995
CURSSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
                                                                                                                                                                                                                         79.6%; Score 86; DB 1; 76.5%; Pred. No. 3.5e-05;
                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/294,859
FILING DATE: 29-AUC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKEY NUMBER: 2803-0003.10
TELECOMMNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08481676
Patent No. 5744584
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  1 DCPSDWSSYEGHCYRVF 17
                                                                                                                                                                                                                                                                                                            1 DCPSEWSSYEGFCYKPF 17
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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TELEFAX: (202) 887-0763
                                                                                                LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
COLOGY: linear
US-08-294-859-2
                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.5#
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 117 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: single
linear
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Gaps
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GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Forby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Femple University - Of The Common-
ADDRESSEE: Wealth System of Higher Education
STREET: 406 University Services Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education STREET: 406 University Services Building CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  COUNTEY: U.S.A.

ZIP: 19122

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUW TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

APPLICATION NUMBER: US/07/893,929

FILING DATE: December 3, 1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DCPSEWSSYEGFCYKPF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEEX: No. 533667e
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.6%;
Best Local Similarity 76.5%;
Matches 13; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 123 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                        Pennsylvania
                                                                                                                                                                                                                                                                       Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-893-929A-4
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Gaps

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DCPSDWSSYEGHCYRVF 17

RESULT 6 US-07-893-929A-4

1 DCPSEWSSYEGFCYKPF

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13; Conservative

Matches

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Gaps
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                77.8%; Score 84; DB 1; Length 50; 76.5%; Pred. No. 2.8e-05; ive 2; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: Morrison & Foerster STREET: 2000 Pennsylvania Ave. N.W., Suite 5500 CITY: Washington, D.C. COUNTY: USA ZIP: 20006-1888
ZIP: 20006-1888
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATER: PC-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DO
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APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-481-676-5
Sequence 5, Application US/08481676
Sequence 5, Application US/08481676
Patent No. 744584
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INFURITION: ANTITHROMEOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GAPPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murashige, Rate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMULICATION INFORMATION:
TELEFHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-294-859-5
; Sequence 5, Application US/08294859
; Patent No. 5679542
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington, D.C. COUNTRY: USA ZIP: 20006-1888
                         Query Match
Best Local Similarity 76.55
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614,443A
FILING DATE: 19901116
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORM
                         OCHEATING SYSTEM: MS-DOS
SOPTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY, AGENT INFORMATION:
NAME: MODIACO, DATIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-614-443A-5

Sequence 5, Application US/07614443A

Patent No. 5342030

GENERAL INFORMATION:
APPLICANT: SCARBOROUGH ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
STATE: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DCPSDWSSYEGHCYRVF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: None
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acids
STRANDEDNESS: single
IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-07-614-443A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
PCT-US92-10344-4
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Query Match 76.9%; Score 83; DB 2; Length 126; Best Local Similarity 70.6%; Pred. No. 9.9e-05; Matches 12; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-612-840A-2
                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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APPLICANT: YAMAMOTO, HIROSHI
APPLICANT: MAGANO, Mitsuyo
APPLICANT: KITO, MORIKAZU
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TSUNIK, KOICHI
APPLICANT: SOSHINOTO, RYOCA
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
CORRESPONDENCE ADDRESS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
F: 1755 S. Jefferson Davis Highway, Suite 400
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.8%; Score 84; DB 1; Length 50; ilarity 76.5%; Pred. No. 2.8e-05; Conservative 2; Mismatches 2; Indels
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

DERAITING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,676

FILING DATE: 07-UN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/294,859

FILING DATE: 29-AUG-1994

ATYORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29,959

TELECOMMONICATION INFORMATION:

TELECOMMONICATION INFORMATION:

TELERAX: (202) 887-160

TELERAX: (202) 887-160

TELERAX: 90-4030

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LUNGTH: SECONDER SECOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 2220
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5856126man F. Oblon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 5856126man F. Oblon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DCPSDWSSHEGHCYKVF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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CITY: Ar
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APPLICANT: NGANO, MITEUYO
APPLICANT: KITO, MOCKIKAZU
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TSOBAYASHI, KOICHI
APPLICANT: YOSHIMOTO, RYOTA
APPLICANT: YOSHIMOTO, RYOTA
APPLICANT: YOSHIMOTO, RYOTA
APPLICANT: WITHER APPLICANT: THEOMBUS ACTIVITY AND TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                     76.9%; Score 83; DB 2; Length 38; 70.6%; Pred. No. 2.9e-05; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Veration 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MRX-1996
CLASSIFICATION NUMBER: UF 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Nacyuki
APPLICANT: YAMAMOTO, Hiroshi
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ECPSGWSSYDRYCYKPF 19
                                                                                                                                                                                                                                                                                                                                                                                                                          1 DCPSEWSSYEGFCYKPF 17
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                            : 38 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 126 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                  Query Match 76.9
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-840A-1
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; MOLECULE TYPE: peptide
US-08-612-840A-2
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Pred. No. 0.0001;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPETATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: PAPLICATION DATA:
APPLICATION NUMBER: US/08/481,676
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/294,859
FILING DATE: 129-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H:
NAME: Murashige, Kate H:
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08481676
Sequence 1, Application US/08481676
Patent No. 5744584
GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVERTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
                                                                           CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.9%; Score 83;
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
                                                                                                                                                                                                                    TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.6'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-481-676-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614,443A
FILING DATE: 19901116
CLASSIFICATION: 530
                                                                                                                                                                                                                          APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22803-20003.00
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 Sequence 1, Application US/07614443A; Patent No. 5342830; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: MALESHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2280:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415,
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TWOTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ECPSGWSSYDRYCYKPF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DCPSEWSSYEGFCYKPF 17
                                    1 DCPSEWSSYEGFCYKPF 17
                                                         ECPSGWSSYDRYCYKPF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-07-614-443A-1
                                                                                                                                  RESULT 13
US-07-614-443A-1
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Gaps

0; Gaps Best Local Similarity 70.6%; Pred. No. 0.0001; Matches 12; Conservative 3; Mismatches 2; Indels

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1 DCPSEWSSYEGFCYKPF 17
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3 ECPSGWSSYDRYCYKPF 19

ð D D Search completed: December 8, 2003, 09:56:26 Job time : 4.69143 secs

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Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 95, Appli
                                                                                                                                                                                                                   December 8, 2003, 09:54:55; Search time 6.99429 Seconds (without alignments) 452.044 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-969-763-3

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US-09-929-230-2

US-09-96-763-1

US-09-96-763-1

US-09-929-230-8

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US-09-929-230-8

US-09-929-95
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Maximum Match 100%
Listing first 45 summaries
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1 DCPSEWSSYEGFCYKPF 17
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Maximum DB seg length: 200000000
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Sequence 231, App Sequence 422, App Sequence 422, App	THE SNAKE
15 US-10-125-540-302 10 US-09-978-295A-231 110 US-09-978-192A-231 110 US-09-978-192A-231 111 US-09-978-182A-231 111 US-09-978-184-231 111 US-09-978-184-231 111 US-09-978-194A-231 112 US-09-978-194A-231 113 US-09-978-194A-231 114 US-09-978-194A-231 115 US-09-978-194A-231 11 US-09-978-194A-231 12 US-09-978-194A-231 12 US-09-978-194A-231 13 US-09-978-194A-231 14 US-09-978-194A-231 15 US-09-978-194A-231 17 US-09-978-194A-231 18 US-09-978-194A-231 18 US-09-978-194A-231 19 US-09-978-194A-231 10 US-09-978-194A-231 11 US-09-978-194A-231 12 US-09-978-194A-231 12 US-01-140-014-422 12 US-10-140-471-422	GNMENTS "XY Li, Xin Cheng, ", Man-Zhi Huang, kong, Yan Liu and OMBOSIS ENZYME FROM GKISTRODON ACUTUS reet e, 1.44 Mb c, DOS 5.0 dows 2.0 /938,114
	ion US/099381 003022350A1 003022350A1 00310, Li-We nn-Guo Liu, Li-We nn-Guo Ding, E il-Ran Chen NTION: AN AN NTION: AN NTION: AN NTION: AN NTION: AN NTION DATA: TION NUMBER: U ATE: 23-Aug-2 CATION DATA: TION NUMBER: U ATE: 23-Aug-2 CATION DATA: TION NUMBER: U ATE: CATION DATA: TON NUMBER: U ATE: CURLON NUMBER: U
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FILING DATE: «UDKIDOWD)
ATTORNEY/AGENT INFORMATION:
NAME: Chen, Anthony C.
NAME: CHEN, ANTHONY C.
REFERENCE/DOCKET NUMBER: 233/298

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APPLICANT: SHIMBA, NOBUHISA
APPLICANT: YAMADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%; Score 81; DB 11;
llarity 76.5%; Pred. No. 9.9e-05;
Conservative 1; Mismatches 3;
                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,114
FILING DATE: 23-Aug-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
RAPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 214760US0
CURRENT APPLICATION NUMBER: US/09/969,763
CURRENT FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: JP 2000-305279
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-938-114-3
                   k Lyon
Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Chen, Anthony C. REGISTRATION NUMBER: 38,673
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Sequence 10, Application US/09969763
Publication No. US20020198363A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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               ADDRESSEE: Lyon & 1
STREET: 633 West Fi
Suite 4700
                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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KAYAHARA, TAKASHI
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ISHIKAWA, KOHKI
SUZUKI, EIICHIRO
GONDOH, KEIKO
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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LENGTH: 110
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APPLICANT:
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APPLICANT: YAMADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING FILE REFERENCE: 214760US0
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                                                                                                                                                                                                                                                                                              100.0%; Score 108; DB 11; Length 17; 100.0%; Pred. No. 8.9e-09; tive 0; Mismatches 0; Indels (
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Publication No. US20030022350A1
GENERAL INFORMATION:
APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng,
Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
Jin-Guo Ding, Fang Rong, Yan Liu and
Hui-Ran Chen
                                                                                                                                         TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/969,763 CURRENT FILING DATE: 2000-10-25
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PRIOR APPLICATION NUMBER: JP 2000-305279
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Version 3.1
                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09969763
Publication No. US20020198363A1
                                                                           INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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KAYAHARA, TAKASHI
FUTAKI, FUMIE
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SUZUKI, EIICHIRO
GONDOH, KEIKO
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Best Local Similarity 100.C
                                                           TELEX: 67-3510
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Best Local Similarity
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US-09-938-114-3
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ORGANISM: ARTIFICIAL SEQUENCE

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20 DCPSDWSSYDQHCYKVF 36
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                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Sistrurus miliarius
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KAYAHARA, TAKASHI
FUTAKI, FUMIE
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                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.6
Matches 12; Conservative
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Best Local Similarity 70.6
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                        LENGTH: 151
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            RESULT 6
US-09-929-230-2
                                                                                                                                                                                                                                                                                                                                                US-09-929-230-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-226-420-2
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APPLICANT:
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                                                       ch 75.0%; Score 81; DB 10; Length 110; Il Similarity 70.6%; Pred. No. 0.00034; 12; Conservative 2; Mismatches 3; Indels
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Pred. No. 0.0004;
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and Hui-Ran Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECORPOTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASESEQ for Windows 2.0
SOFTWARE: FASESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,114
FILING DATE: 23-Aug-2001
CLASSIFICATION: clunknown>
APPLICATION NUMBER: 09/058,740
FILING DATE: clunknown>
APPLICATION NUMBER: 09/058,740
FILING DATE: clunknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chen, Anthony C.
RECISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 180PRATION:
TELECOMMUNICATION 180PRATION:
TELECOMMUNICATION 180PRATION:
TELECOMMUNICATION 180PRATION:
TELECOMMUNICATION 180PRATICE:
SEQUENCE CHRACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 633 West Fifth Street
; OTHER INFORMATION: SYNTHETIC PEPTIDE US-09-969-763-10
                                                                                                                                                                                                                                                                          Sequence 2, Application US/09938114 Publication No. US20030022350Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                            3 ECPSGWSSYSRYCYKPF 19
                                                                                                                                        1 DCPSEWSSYEGFCYKPF 17
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1 Similarity 76.5%;
13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
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Best Local Similarity
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                                                       Query Match
Best Local S
Matches 12
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17

1 DCSSDWSSYEGHCYKVF 17

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TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING THE
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                                                                                                                                                                                                                                                                                                                     72.2%; Score 78; DB 10; Length 15:
70.6%; Pred. No. 0.0012;
Mismatches 3; Indels
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Patent No. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILLE REFERENCE: 00-72
CURRENT FILING DATE: 2001-08-13
NUMBER: PASE IN NOS: 14
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REPERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASELSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09969763
Publication No. US20020198363A1
GENERAL INFORMATION:
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SUZUKI, EIICHIRO
GONDOH, KEIKO
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APPLICANT:
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1 DCPSEWSSYEGFCYKPF 17
                     24 DCPSGWSSYDQHCYRVF 40
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US-10-226-420-8
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; ORGANISM: Sistrurus miliarius
US-09-929-230-8
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Best Local Similarity 53.3%;
Matches 8; Conservative
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Matches 8; Conserv
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US-09-929-230-8
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                                                                                                                                                                                                                                          68.5%; Score 74; DB 10; Length 126; illarity 64.7%; Pred. No. 0.0038; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10226420;
Publication No. US20030157686A1
| GENERAL INFORMATION:
| APPLICANT: Sheppard, Paul O. |
| TITLE OF INVENTION: RATTLEENAKE VENOM GLAND PROTEINS FILE REFERENCE: 00-72 CURRENT APPLICATION NUMBER: US/10/226,420;
| CURRENT FILING DATE: 2002-08-21;
| NUMBER: PSECSEQ ID NOS: 14
| SOFTWARE: FaetSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-929-230-5

Sequence 5, Application US/09929230

Fatent No. US2002161203A1

GRANEAL INFORMATION:

APPLICANT: Sheppard, Paul O.

TILLE OF INVENTION:
FILE OF INVENTION RATILESNAKE VENOM GLAND PROTEINS

FILE PERFERENCE: 00-72

CURRENT APPLICATION NUMBER: US/09/929,230

CURRENT FILING DATE: 2001-08-13

NUMBER OF SEQ ID MOS: 14

SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                   CURRENT APPLICATION NUMBER: US/09/969,763
CURRENT FILING DATE: 2000-10-25
PRIOR PELLING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 126
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DCPSGWSSYDQHCYRVF 40
                                                                                                                                                                                                                                                                                                                                              3 ECPSGWSSTDRYCYKPF 19
                                                                                                                                                                                                                                                                                                                     1 DCPSEWSSYEGFCYKPF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-5
                                                                                                                                                                                       ; ORGANISM: Crotallus horridus
US-09-969-763-1
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   FILE REFERENCE: 214760USO
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserva
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US-10-226-420-5
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ENGINT 11

US 929-20-0

SEGURT 11

US 929-20-0

SEGURT 21

US 929-20-0

SEGURT 21

US 929-20-0

SEGURT 21

US 929-20-0

SEGURT 21

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Search completed: December 8, 2003, 10:07:06 Job time : 6.99429 secs
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US-09-751-708A-95

i Sequence 59, Application US/09751708A

i Sequence 50, Application US/09751708A

i Sequence 50, Application US/09751708A

i GENERAL INFORMATION:

i APPLICANT: TERMAN, David S

i TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

i FILE REFERENCE: 751708

i CURRENT APPLICATION NUMBER: US/09/751,708A

i CURRENT APPLICATION NUMBER: US 60/173,371

i REMORE: PRIOR FILING DATE: 1999-12-28

i NUMBER OF SEQ ID NOS: 166

i SEQ ID NO 95

i LEWGTH: 1456

i TYPE: PRT

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Fatent No. US20020042386A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 302
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                         Query Match 56.5%; Score 61; DB 10; Length 1456; Best Local Similarity 64.3%; Pred. No. 2.6; Matches 9; Conservative 1; Mismatches 4; Indels
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; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 CPSQWWPYAGHCYK 375
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362 CPSQWWPYAGHCYK 375
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Best Local Similarity 61.5
Matches 8; Conservative
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US-09-764-870-302
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AY233866 Deinagkis
AF176421 Deinagkis
AY091761 Deinagkis
AF350324 Deinagkis
AB036881 Deinagkis
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AX097760 Deinagkis
AR176420 Deinagkis
D8331 Trimeresuru
AB046491 Trimeresuru
X16349 Crotalus du
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AF125310 Gloydius
AR02653 Sequence
AX404807 Sequence
BD143687 Protein h
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AF102902 Deinagkis
AB019615 Agkistrod
AX427204 Sequence
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Deinagkis
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AX427203 Sequence
AF463521 Deinagkis
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                                                                                                                                                                                                                                                                                                                                                                        Gloydius
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AF102901 Deinagkis
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J05550 Human manno
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AL935252 Lactobaci
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AB036880 I
AF190827 G
AF387100 I
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-MODEL=frame+_p2n.model -DEV=xlh
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-DB=GenEmbl - USPTO_spool/US09938114/runat_0812600_1-LCOPECL=0 -LCOPECL=0 -LCOPECL=0
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                                                                                                                                                                                                                                                          5777422
   GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                           - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                             2888711 seqs, 20454813386 residues
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                           108
1 DCPSEWSSYEGFCYKPF 17
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Query Match:
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109 c 117 t
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Deinagkistrodon acutus clone 2100488 agkisacutacin B-chain mRNA,
            PAT 20-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished

2 (bases 1 to 478)

2 (bases 1 to 478)

2 W.H., Xiang,K., Wang,Y. and Liu,J.

Direct Submission

Submitted (22-MAR-2002) Dept. of Biochemistry and Molecular

Biology, University of Science and Technology of China, School of

Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China

Location/Quallfiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinagkistrodon acutus
Deinagkistrodon acutus
Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
(bases 1 to 478)
Yu, H., Xiang, K., Mang, Y. and Liu, J.
E chain of agkisacutacin from Deinagkistrodon acutus
                                                                                                                Unclassified.

1 (bases 1 to 454)

Li,B.X. and Cheng,X.

Antithrombosis enzyme from the snake venom of agkistrodon acutus Patent: US 6489451.A 12 03-DEC-2002;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      10 others
             linear
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16
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/note="C-type lectin family member"
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Matches:
Conservative:
Mismatches:
Indels:
             DNA
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          ARZS9041 454 bp Sequence 12 from patent US 6489451.
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                                                                                                                                                                                                                /organism="unknown"
107 c 114 a
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                                                         GI:27309526
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AR259041
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                                                                                                                                                                                                                                                                                                                                           Deinagkistrodon acutus
Deinagkistrodon acutus
Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
1 (bases 1 to 369)
Zha,X.D., Ren,B., Liu,J. and Xu,K.S.
Genomic DNA sequence of b chain of Agkissain, a C-type lectin-like genomic DNA sequence of b chain of Agkissain, a detype lectin-like significance.
                                                                                                                                                                                                                                                                 VRT 09-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
2 (bases 1 to 369)
2 (bases 1 to 369)
2 (bases 1 to 36)
Direct Submission
Submitted (07-MAY-2003) Biology, School of Life Science, Anhui University, 3 Feixi Road, Hefei 230039, China
Location/Qualifiers
                                                                                                                                                        17
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Deinagkistrodon acutus agkisasin-b gene, partial cds.
AY293866
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115
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478
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    .369
    .7oganism="Deinagkistrodon acutus"
/mol type="genomic DNA"
/db_xref="taxon:36307"

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/product="agkisasin-b"
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                     AUTHORS
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AF350324
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                                                                        Deinagkistrodon acutus
Deinagkistrodon acutus
Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
1 (bases 1 to 458)
1 (bases 1 to 458)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="agkisacutacin consists of two heterologous subunits
(A and B chains) linked by an inter-subunit disulfide
bond"
AF176421 VRT 19-JAN-2000 Deinnear URT 19-JAN-2000 AF176421 AF176421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MGRFIFVSFGLLVVFLSLSGTAADCPSDMSSYEGHCYRPPBERK
TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLWHIGLKNIWNGCYWKW
SDGTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCKFQA"

109 c 116 g 115 t
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                                                                                                                                                                                                                                                                                                   Submitted (08-AUG-1999) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, School of
Life-Science, Huangshan Road, Hefei, Anhui 230027, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinagkistrodon acutus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
1 (bases 1 to 978)
Yu.H., Xiang,K., Wang,Y. and Liu,J.
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Deinagkistrodon acutus clone 2101 ACF 1/2 B-chain mRNA, complete
                                                                                                                                                                                                         Agkisacutacin, a new fibrinolytic & anti-platelet protein from Agkistrodon acutus venom
Unpublished
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/organism="Deinagkistrodon acutus"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                    2 (bases 1 to 458)
Cheng, X., Liu, J., Li, B.X.Y. and Qian, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/tissue_type="venom"
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AY091761.1 GI:20562942
                                             AF176421.1 GI:6715114
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AY091761
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SNAAMLKTTURAEBSTYSTNIKRRSITCRMIANFVCEFQA"
107 c 125 cv 719 t
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STEEADFVVKLAFQTFDYG1FWMGLSNIWNQCNWQWSNAAMLKYTDWAEESYCVYFKS
TNNKWRSITCRMIANFVCEFQA"
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2 (bases 1 to 478)
Yu,H., Xiang,K., Wang,Y. and Liu,J.
Direct Submission
Submisted (12-MAR-2002) Dept. of Biochemistry and Molecular
Biology, University of Science and Technology of China, School of
Life Science, Ruangshan Road, Hefei, Anhui 230027, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="IX/X-BP family member; coagulant and anticoagulant"
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Deinagkistrodon acutus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
Zha,X. and Xu,K.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GATTGTCCTCTGATTGGTCTCCTATGAAGGCCATTGCTACAAGCCCTTC 120
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Deinagkistrodon acutus agkisasin-b mRNA, complete cds.
AR350324
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/note="C-type lectin family member"

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/organism="Deinagkistrodon acutus"
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/mol_type="mRNA"
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/lab_host="Escherichia coli JM109"
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Mismatches:
Indels:
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Matches:
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/product="ACF 1/2 B-chain"
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74 GATTGTCCTTCTGATTGGTCCTCTATGAAGGGCATTGCTACAAGCCCTTC 124
                             1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
US-09-938-114-4 (1-17) x AB036881 (1-592)
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Pred. No.:
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Ogawa, T. and Tani, A.

Direct Submission

Submitted (14-JAN-2000) Tomohisa Ogawa, Tohoku University, Graduate School of Agricultural Science; 1-1, Tsutusmidori Amamiyamachi, Abba-ku, Sendai 991-8555, Japan (E-mail:ogawa@biochem.tohoku.ac.jp, URL:http://www.agri.tohoku.ac.jp/hoozo/, Tel:81-22-717-8808,
                                                                                                                                                                                                                                              ABUJEBBI 592 bp mRNA linear VRT 23-MAY-2002 Deinagkistrodon acutus acp-b mRNA for anticoagulant protein-B, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB20441.1"
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SNAAMLKYTDWAEBSYCVYFKSTNNKWRSITCRMIANFVCEFQA"
                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata; Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Deinagkistrodon.
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                                                                                                                                                                    1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
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                                                                                                                                                                                        GATTGTCCTTCTGATTGGTCCTCTTATGAAGGCATTGCTACAAGCCCTTC
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/product="anticoagulant_protein-B"
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Matches:
Conservative:
Mismatches:
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Gaps:
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Mismatches:
Indels:
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Matches:
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/db_xref="taxon:36307"
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Deinagkistrodon acutus
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/gene="acp-b"
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Best Local Similarity:
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                         Alignment Scores:
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DB:
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AB036881
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                                        No.:
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                         ACCESSION
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KEYWORDS
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                                                      Score:
                                     Pred.
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AF244901 438 bp mRNA linear VRT 29-JUN-2000 Calloselasma rhodostoma aggretin beta chain mRNA, partial cds. AF244901 GI:8809813
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/podon_refactor_IX/factor_X binding protein B chain"
/protein_id="BAA11888.1"
/db_xref="G1:1402642"
/db_xref="G1:1402642"
/tb_xref="G1:1402642"
/db_xref="G1:1402642"
/db_xref="G1:1402
                  VRT 06-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Inpidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.

    (Dases 1 to 698)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
698 bp mRNA linear VRT 06-FEE Trimeresurus flavoviridis mRNA for factor IX/factor X binding procein B chain, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsuzaki, R., Yoshiara, E., Yamada, M., Shima, K., Atoda, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-PEB-1996) Takashi Morita, Meiji College of Biochemistry: 1-22-1 Yatocho, Tanashi, Tokyo 188, Japan (Tel:0424-21-0101(ex.429), Fax:0424-21-1489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
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/organism="Trimeresurus flavoviridis"
/mol_type="mRNA"
Xref="taxon:88087"
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factor IX/factor X binding protein B chain.
Trimeresurus flavoviridis
Trimeresurus flavoviridis
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein from snake venom
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88.24%
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185 c
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Direct Submission
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/protectin_id="AAC38522"."

/db_xref="G1:11066256"."

/db_xref="G1:11066256"."

/db_xref="G1:11006256"."

/db_xref="G1:110
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ei-Shan, Tao-Yuan, Taiwan
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Molecular structure and functional characterization of agglucetin,
a tetrameric glycoprotein Ib-binding protein, from Formosan pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 bp mRNA linear VRT 26-SEP-20
Deinagkistrodon acutus agglucetin-beta 1 subunit precursor, mRNA,
Complete cds.
AF540647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Deinagkistrodon.
                Submitted (22-OCT-1999) Cardiovascular center, Yonsei University College of Med., 134 Shinchon-dong, Seoul 120-752, Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 688)
Wang, W.J. and Huang, T.F.
A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist
Thromb. Haemost. 86 (4), 1077-1086 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GATTGTCCCTCTGGTTGGTCCTCCTATGAAGGCATTGCTACAAACCATTT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                                                                                                              24. 464 / Inote="coagulation factor Xa inhibitor"
                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="halyxin_B-chain precursor"
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Wang.W.-J., Ling.Q.-D. and Huang,T.-F.
Direct Submission
Submitted (23-AUG-2002) Department of Nursing, of Technology, 261, Wen-Hwa I Rd., Kwei-Shan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Deinagkistrodon acutus"
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Mismatches:
Indels:
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/product="halyxin B-chain"
a 142 c 157 g 155 t
                                                                                                                                                    organism="Gloydius halys"
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                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:8714"
                                                                                                                                                                                                                                  tissue_type="venom"
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                                                                                                    Location/Qualifiers
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Best Local Similarity:
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m viper}
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                   JOURNAL
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TITLE
JOURNAL
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                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 438)
Chung,C.H., Au,L.C. and Huang,T.F.
Direct Submission

Submitted (11-MAR-2000) Pharmacology, College of Medicine, National Taiwan University, No. 1, Sec. 1, Jen-Ai Rd., Taipei, Taiwan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="aggretin beta chain"
/protein_id="AAR79553.1"
/db_xxef="G1:8809814"
/translation="MGRFIFVSFGLLVVFLSLSGTGADCPSGWSSYEGHCYKPFNEPK
NWADARRFCKLOPKHSHLVSFQSAEEADFVVKLTRPRLKANLVWMGLSNIWHGCNWQW
SGGARLNYKDWQGQSECLAFRGVHTFWLNMDCSSTGSFVCKFKA"
100 c 101 g 109 t
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                                                                           Eukaryotta, Metazooa, Churdata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata; Scleroglossa, Serpentes, Colubroidea, Lopidosauria, Calioselasma.

(Dases 1 to 438)

Chung, C.H., Au, L.C. and Huang, T.F.

Molecular cloning and sequence analysis of aggretin, a collagen-like platelet aggregation inducer
Biochem. Biophys. Res. Commun. 263 (3), 723-727 (1999)
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1 (bases 1 to 634)

Koo, B.H., Sohn, Y.D., Kim, D.S., Jang, Y.S. and Chung, K.H.

A Novel Coagulation Factor Xa Inhibitor from Korean Snake (Agkistrodon halys) venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .>438 // /
/note="forms heterodimer of alpha and beta chains; collagen-receptor agonist; induces platlet aggregation; similar to C-type lectins and glycoprotein Ib binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF197915
Gloydius halys halyxin B-chain precursor, mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GATIGICCCTCTGGTIGGTCCTCTATGAAGGCATTGCTACAAGCCCTTC 120
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Sohn, Y.D., Koo, B.H., Kim, D.S., Jang, Y.S. and Chung, K.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Calloselasma rhodostoma"
/mol_type="mRNA"
/db_xref="taxon:8717"
/tissue_type="venom gland"
                                 (Malayan pit viper)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
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                              Calloselasma rhodostoma
                                                          Calloselasma rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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94.00
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Gloydius halys brevicaudus fibrinogen clotting inhibitor B chain AP125310
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/db_xref="G1:4337052"
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SNAAALKYEAWABIYCYYFKSTNNKWSRACRWEAYFVCEFQA"
137 c 150 g 145 t
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Direct Submission
Submitted (01-FEB-1999) Biochemistry, Yonsei University, Seodaemun
ku Shinchon dong 134, Seoul 120-749, Korea
Location/Qualifiers
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Gloydius halys brevicaudus
Eukaryote, Metazos, Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
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Purification and molecular cloning of snake venom fibrin clotting
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TDGTRLSHNAWITESECIAAKTTDNQWLSRPCSRTYNVVCKFQE'
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                 164 t
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                 173 g
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/codon_start=1
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Sakurai, Y. and Fujimura, Y.
Sakurai, Y. and Fujimura, Y.
Direct Submission Sakurai, Nara Medical University,
Department of Blood Transfusion Medicine; Shijo-cho 840, Kashihara,
Nara 634-8522, Japan (E-mail:ysakurai@nmu-gw.cc.naramed-u.ac.jp,
Tel:81-744-22-3011(ex.328), Fax:81-744-29-0771)
                                                                                                                                                                 /translation="WGRVIFYSFGILVVFISISGTAADCPSEWSSYEGHCYXAFKQSK
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SDGTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTYSFVCKFQA"
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
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The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from pakistrodon halys blomhoffii venom
Thromb. Haemost. 79 (6), 1199-1207 (1998)
                                           51. .501
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                                                                                              /codon_start=1
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/product="agglucetin-beta 1 subunit"
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Patent: EP 1195384-A 2 10-APR-2002;
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/tb_yref="G1:21438047"
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Fukuchi,N., Yamamoto,H., Nagano,M., Kito,M., Tanaka,A., Ishii,K., Kobayashi,T. and Yoshimoto,R.
Peptide having anti-thrombus activity and method of producing the
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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    /organism="Crotalus horridus"

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Indels:
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/note="unnamed protein product"
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Patent: US 5856126-A 7 05-JAN-1999;
Location/Qualifiers
                                                                690 bp
Sequence 7 from patent US 5856126.
AR026653
AR026653.1 GI:5937493
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AX404807
AX404807.1 GI:21438046
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180 c 170 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:8747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 g
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crotalus horridus horridus
Crotalus horridus horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
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88.24%
70.59%
76.85%
                                                                                                                                                                                                                                                                                    Unclassified.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 a
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                                                                                                                                                                                                                    Unknown.
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                                                                                                                                                                                                                                                       Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                      DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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ORIGIN
RESULT 14
AR026653
LOCUS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
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Alignment Scores:

```
Pred. No.: 0.000182 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24$ Conservative: 3
Best Local Similarity: 70.59$ Mismatches: 2
Query Match: 6
Best Local Similarity: 70.59$ Mismatches: 2
DB: 6
Conservative: 3
Conservative:
```

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us-09-938-114-4.rng

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

(without alignments)
786.026 Million cell updates/sec December 8, 2003, 12:39:59 ; Search time 58.3829 Seconds - nucleic search, using frame_plus_p2n model OM protein Run on:

US-09-938-114-4 Title: Perfect score:

1 DCPSEWSSYEGFCYKPF 17 Sequence:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

2552756 seqs, 1349719017 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

Database :

(SIDSI)/goddata/genesequj-empl./NAI)989.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)989.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)989.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)990.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)991.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)992.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)994.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)994.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)996.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)996.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)999.DAT:
(SIDSI)/goddata/genesequj-empl./NAI)999.DAT: N. Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| SIDS1/gcgdata/geneseqn-emb1/NA1986.DAT:*
| SIDS1/gcgdata/geneseqn-emb1/NA1988.DAT:*
| SIDS1/gcgdata/geneseqn-emb1/NA1988.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Description	encodir	Snake venom blood Koresh adder snake	ke venom a	encoding	DNA encoding the a Snake venom blood		Pigmy rattlesnake	Figmy rattlesmake	coding	DNA encoding solub	my rattl	Human cDNA encodin	DNA encoaing novel Human polynucleotí	Korean adder snake	Human immune/naema Human polynucleoti	Human polynucleoti	Human PRO/92 nucle Human PRO/92 (UNO4	Human PRO792 nucle	Human PRO792 cDNA		an cDNA end	DNA encoding novel	DNA encoding novel	Snake venom protei		esnake	BOVING EST ASSOCIA Human reproductive	ncoding huma	Human secretion an	reproduct								antithrombosis enzyme beta chain.	:lot;	rodegenerative dis	nromboangiitis obliteran angina: acute thrombosis	vein thrombosis; oedem
SUMMARIES	1																														ABZ24622 AAS31230	ALIGNMENTS			4 BP.			on acutus antith	Antithrombosis; ss; PCR; beta chain; fibrin	enosis; cancer;	ebral thrombosis; tl disease; unstable	embolis stroke:
Length DB																															5085 25 857 22				CDNA; 454		: entrv)	 Deinagkistrodon	; PCR; bet	ion; reste	osis; cere vascular	stenocardia; pulmonary
% Query Match I																															50.9				standard;		3 (first	ing Deina	osis; ss	infarcti	c thrombo cerebral	tenocardi arteria]
Score																									5						55			7.4	93674	ABX93674;	2-JUN-2003	cDNA encoding	ntithromb latelet a	ocardial	anglopathi ischaemic	unstable s peripheral
Result No.	, , ,	M 10	4	u u		60 C	y L	11	122	14	15	16		19	21	22	24.	. 25	27	28	29	31	C 33	4 EU	36	37	9 60	0 4 0	4 4 1 24	43	44 45		HIGGG	ABX93674	ID	·	XX DT 02		KW Ar			

US-09-938-114-4 (1-17) x ABX93674 (1-454)

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The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.005 micro/kg and this activity was increased significantly at 1.0 hour and at 0.11 micro /kg. The composition is useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, angiopathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thromboangiitis obliterans, pulmonary embolism, deep vein thrombosis,
                                                                                                                                                                                                                                                                                                                                                      /note= "Unsequenced region could be 10-20 nucleotides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peripheral arterial occulsion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents CDNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occulusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and
                                                                                                          /transl_except= (pos:216..218,aa:Xaa)
/transl_except= (pos:216..218,aa:Xaa)
/transl_except= (pos:219..221,aa:Xaa)
/transl_except= (pos:222..224,aa:Xaa)
/transl_except= (pos:225..227,aa:Xaa)
/note= "Xaa = unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinagkistrodon acutus antithrombosis enzyme beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 454 BP; 114 A; 107 C; 114 G; 109 T; 10 other;
                                                                                                     *tag= a product= "Antithrombosis enzyme"
                                                                                                                                                                                                                                                                    72..440
/*tag= c
/note= "Mature beta chain"
217..226
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HEFE-) HEFEI SIU FUNG USTC PHARM CO LID.
                                                                                                                                                                                                                                                    note= "Leader peptide"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                             size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0058740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-043886P
                                                                                                                                                                                                                                      *tag= b
                                 Deinagkistrodon acutus.
                                                                                   ..443
*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-352116/33.
P-PSDB; ABU08799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unstable angina
                                                                                                                                                                                                                                                                                                                                                                                                           US6489451-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-1998;
                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                        mat_peptide
thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li BX,
                                                                   Key
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The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used in the treatment of thrombogenesis. The present sequence encodes the B chain of halyxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 GATTGTCCCTCTGGTTGGTCCTCCTATGAAGGCCATTGCTACAAACCATTT 143
                GATTGTCCCTCTGAGTGCTCCTCCTATGAAGGCATTGCTACAAGCCCTTC 122
                                                                                                                                                                                 Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
thrombosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korean adder snake venom salmorin B chain protein cDNA sequence
                                                                                                                                                          Snake venom blood anticoagulant halyxin B chain coding sequence
1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 633 BP; 179 A; 142 C; 157 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633
15
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                        Son YD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                        Koo BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-938-114-4 (1-17) x AAI71877 (1-633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 11; 21pp; Korean.
                                                                              AAI71877 standard; DNA; 633 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL42016 standard; cDNA; 583
                                                                                                                                                                                                                                                                                                                                                                                        DS,
                                                                                                                                                                                                                                                                                                                                     99KR-0025105
                                                                                                                                                                                                                                                                                                         29-JUN-2000; 2000KR-0036591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e-05
94.00
88.24%
88.24%
87.04%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2002 (first entry)
                                                                                                                                   10-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Kim
                                                                                                                                                                                                                                                                                                                                                               (BIOB-) BIOBUD CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-637330/73.
                                                                                                                                                                                                                                                                                                                                                                                        Jung GH,
                                                                                                                                                                                                                            Agkistrodon halys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAM51544.
                                                                                                                                                                                                                                                     KR2001049671-A.
                                                                                                                                                                                                                                                                                                                                     29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                 15-JUN-2001
                                                                                                        AAI71877;
                                                                                                                                                                                                                                                                                                                                                                                        Jang YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL42016
                                                                 AAI71877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                       ð
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454 16 0 10 0

Length:
Matches:
Conservative:
Mismatches:

7.24e-07 101.00 94.12% 94.12% 93.52%

> Percent Similarity: Best Local Similarity: Query Match: DB:

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The invention comprises the nucleotide and protein sequences of a salmorin protein derived from the venom of Korean adder. Salmorin protein is composed of an A chain and a B chain, and has inhibitory activity against fibrinogen clotting. The salmorin protein of the invention is useful for treating thrombosis, as it represses fibrinogen clotting potently by binding to prothrombin and thrombin so as to delay blood coggulation. The present cDNA sequence encodes the Korean adder salmorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New salmorin protein derived from venom of Korean adder Agkistrodon halys brevicaudus, useful for treating thrombosis by repressing fibrinogen clotting through repression of activation of prothrombin
Korean adder; ss; salmorin protein B chain; snake venom; fibrinogen clotting inhibition; thrombosis; prothrombin binding; thrombin binding; blood coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                           76.441
/*tag= c
/note= "Mature Salmorin B chain protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 583 BP; 151 A; 137 C; 150 G; 145 T; 0 other;
                                                                                                            /*tag= a
/product= "Salmorin B chain protein"
                                                                                                                                                 '*tag= b
'note= "Signal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-938-114-4 (1-17) x AAL42016 (1-583)
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ89309 standard; cDNA; 690 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1B; 30pp; English.
                                                    Agkistrodon halys brevicaudus.
                                                                                                                                                                                                                                                                                                                                           26-JUL-2001; 2001WO-KR01277.
                                                                                                                                                                                                                                                                                                                                                                     27-JUL-2000; 2000KR-0043470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.000487
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82.35%
82.35%
77.78%
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571..583
/*tag= e
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                                                                                                                                                                                                                      445..570
                                                                                                                                                                                                                                                                                                                                                                                                                            Chung K, Kim D, Koh Y;
                                                                                            7..444
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                 (BIOB-) BIOBUD CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-241907/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAO14521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain protein
                                                                                                                                                                                                                                                                                     WO200214514-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                      sig peptide
                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                 21-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ89309
ð
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583 0 0 0 0

Length: Matches: Conservative: Mismatches:

Indels: Gaps:

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AAR71978 and AAR71979 are snake venom derived antithrombotic peptides, specifically from the snake venom oligopeptide AAR71981, encoded by AAQ89309. These peptides have the advantage of avoiding significant thrombocytopenia when administered at the minimum dose, for in vivo inhibition of platelet von Willebrand factor binding.

(Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Subunit peptide production, snake venom, rattlesnake, thrombolytic, von Willebrand's factor; blood platelet-inhibitory activity; ds.
                                                                     Antithrombotic peptide; snake venom; platelet binding inhibition; von Willebrand factors; Crotalus horridus horridus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GAATGTCCCTCCGGTTGGTCTTCCTATGATGGTATAGCTACAAGCCCTTC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                   Single-chain antithrombotic peptide - obtained by cleaving an oligopeptide from snake venom to break inter-chain disulphide bonds but preserve intra-chain disulphide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      690
112
3
2
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                                                                                                                                                                                                                                                                                                           Kobayashi T, Nagano
oto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                             Snake venom antithrombotic oligopeptide cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a snake venom derived protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Pages 47-48; 84pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-938-114-4 (1-17) x AAQ89309 (1-690)
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       Yoshimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                             Kito M,
                                                                                                                                                                                                                                    94WO-JP01555
                                                                                                                                                                                                                                                            93JP-0236975
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          (updated)
(first entry)
                                                                                                           Crotalus horridus horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00086
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88.24%
70.59%
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                                                                                                                                               66..515
                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                      Yamamoto H,
                                                                                                                                                                                                                                                                                   (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                              WPI; 1995-139559/18.
                                                                                                                                                                                                                                                                                                          Fukuchi N, Ishii K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR71981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                  21-SEP-1994;
           25-MAR-2003
                                                                                                                                                                                   WO9508573-A1
                                                                                                                                                                                                                                                          22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2001
                        28-NOV-1995
                                                                                                                                                                                                            30-MAR-1995
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                                                                                                                                                                                                                                                                                                                        ranaka A,
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/product= "Antithrombotic wild-type rattlesnake protein"
                                                                                                                                                                                                                                                    Kito M,
Shimba N,
                                                                                                                                                                                                                                                                                                                    WPI; 2002-364482/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                       P-PSDB; AA020974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombosis; ds.
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                                           EP1195384-A1
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                                                                                     10-APR-2002
                                                                                                                                                                                                                                                      Fukuchi N,
                                                                                                                                                                                                                                                                          Gondoh K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI71876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a method for the production of a subunit peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its subunit using a protein denaturing these denaturing the protein or its agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity on von Willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents DNA encoding rattlesnake protein used in an example illustrating the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake; antithrombotic; glycoprotein Ib; long half life; low antigenicity; drug efficacy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                             Producing physiologically-active subunit peptides originating in polymer proteins by denaturation and specific separation, with lower antigenicity but improved solubility and stability, e.g. blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 GAATGICCCTCCGGTTGGTCTTCCTATGATCGGTATTGCTACAGCCCTTC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding the antithrombotic wild-type rattlesnake protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
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112
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Mismatches:
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                                                                                                                                                                                                                                                           Kayahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 46; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                         Kito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                        platelet-binding inhibitors
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                                                                                                                              2000WO-JP02127
                                                                                                                                                                        99JP-0096073
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    Crotalus horridus horridus.
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76.85%
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/*tag=
                                                                                                                                                                                                                 (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                         N, Kageyama S,
                                                                                                                                                                                                                                                                                                  WPI; 2000-664985/64.
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY85628
                                             WO200059926-A1
                                                                                                                              31-MAR-2000;
                                                                                                                                                                        32-APR-1999;
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Pred. No.:
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                                                                                       12-OCT-2000
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                                                                                                                                                                                                                                                           Fukuchi
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The invention relates to a glycoprotein Ib-binding protein, originating from snake venom, comprising specific mutations and antithrombotic activity. Glycoprotein Ib-binding protein is used in a drug having antithrombotic activity. Glycoprotein Ib-binding protein has a high binding activity to glycoprotein Ib-binding protein has a high binding activity to glycoprotein Ib, a long half life/drug efficacy retention in blood, and low antigenicity. This polynucleotide sequence represents DNA of the wild-type rattlesnake protein of the invention.
                                                                                                                                                                                                                                                                                                                         мопал
                                                                                                                                             Ishikawa K, Suzuki E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein Ib-binding protein, useful for treating thrombosis, comprises specific mutations in protein originating from snake v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snake venom blood anticoagulant halyxin A chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
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112
22
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Matches:
Conservative:
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Indels:
Gaps:
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                                                                                                                                               Futaki F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koo BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-938-114-4 (1-17) x AAK99834 (1-690)
                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 25; 49pp; English
                                                                                                                                               Kayahara T,
                                                                                                                                                                         Yamada N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       вЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI71876 standard; DNA; 601
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04-OCT-2001; 2001EP-0123277
                                            04-OCT-2000; 2000JP-0305279
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88.24%
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                                                                                                (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOB-) BIOBUD CO LTD.
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The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence
                                           Halyxin as blood anticoagulation protein separated from snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pigmy rattlesnake, venom gland protein; blood coagulation; therapy; platelet aggregation; gene; Zsnk2; ds.
                                                                                                                                                                                                                                                                                                                            93 GATTGTCCCTCTGGTTGGTCCTCTATGAAGGGCATTGCTACAACATCTTC 143
                                                                                                                                                                                                                                                                                                     1 AspCysProSerGluIrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "CDS does not include start codon"
                                                                                                                                                             Sequence 601 BP; 166 A; 133 C; 163 G; 139 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pigmy rattlesnake venom gland protein, Zsnk2 gene.
                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Mature Zsnk2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Zsnk2 protein"
                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                              US-09-938-114-4 (1-17) x AAI71876 (1-601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                         encodes the A chain of halyxin.
                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                   Claim 1; Page 9; 21pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-225072P.
2000US-225087P.
2000US-225489P.
2000US-225490P.
                                                                                                                                                                                                                                                                                                                                                                         AAD32053 standard; DNA; 483
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3..458
/*tag=
          WPI; 2001-637330/73.
P-PSDB; AAM51543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sistrurus miliarius.
                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5-AUG-2000;
                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                AAD32053;
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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601 13 0 0 0 0

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system. The polypeptides, which affect blood coagulation and platelet aggregation system, are useful in therapy and diagnostics. The polypeptides are also useful as an educational tool in laboratory protein chemistry and antibody production and analysis. The polymeptide can be used as standards or as unknowns for testing purposes. The polypeptides are also useful in identifying protein by western blotting, protein purification, determining the weight of expressed polypeptides as a ratio to total protein expressed, identifying peptide cleavage sites, coupling amino and carboxyl terminal tags, mass spectrometry, circular dichroism to determine conformation or sequencing. The present sequence is Sistrurus miliarius venom gland protein, Zsnk2 gene.
                                                which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; gene; Zsnk3; ds.
                                                proteins,
                                            New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, affect blood coagulation and platelet aggregation system, useful therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 GATTGTCCCTCTGACTGGTCCTCCTATGATCAGCATTGCTACAAGGTCTTC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 483 BP; 129 A; 112 C; 123 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             483
22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product= "Mature Zsnk3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product= "Zank3 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-114-4 (1-17) x AAD32053 (1-483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                       Claim 5; Page 71-72; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        721
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/*tag= b
160..546
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.00
82.35%
70.59%
72.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91..549
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
WPI; 2002-269180/31.
P-PSDB; AAE20178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sistrurus miliarius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD32055 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
                                                                                         molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200214364-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD32055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
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0
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13-AUG-2001; 2001WO-US25310

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
practical kits for courses related to genetics and molecular biology,
corporal kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The
polymclectide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
corporations blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing, The present sequence is Sistrurus miliarius venom gland
                                                                                                                                                                                                                                       New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pigmy rattlesnake venom gland protein Zsnk2, degenerate nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pigmy rattlesnake, venom gland protein; blood coagulation; therapy; platelet aggregation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 721 BP; 192 A; 167 C; 203 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-938-114-4 (1-17) x AAD32055 (1-721)
                                                                                                                                                                                                                                                                                                                              Claim 5; Page 73-74; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD32054 standard; DNA; 453 BP
              2000US-225072P.
2000US-225087P.
2000US-225489P.
2000US-225490P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0725
71.00
76.47%
64.71%
65.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                     (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                       Sheppard PO, Bishop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sistrurus miliarius.
                                                                                                                                                                                        WPI; 2002-269180/31.
P-PSDB; AAE20179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                               molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200214364-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                  14-AUG-2000;
14-AUG-2000;
                                                                 15-AUG-2000;
20-DEC-2000;
                                                    15-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
practical kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The
polynucleotide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
proteins by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
protein Zsnk2, degenerate nucleic acid.
                                                                                                                                                                                                                                      which
                                                                                                                                                                                                                                    New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, wh affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 453 BP; 74 A; 32 C; 84 G; 70 T; 193 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pigmy rattlesnake venom gland protein, Zsnk4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3..437
/*tag= a
/product= "Zsnk4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                       Disclosure; Page 72-73; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             platelet aggregation; gene; Zsnk4; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-938-114-4 (1-17) x AAD32054 (1-453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                               2000US-225087P.
2000US-225489P.
2000US-225490P.
2000US-356997P.
13-AUG-2001; 2001WO-US25310.
                                 2000US-225072P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD32057 standard; DNA; 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.256
66.00
64.71%
52.94%
61.11%
                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                    Sheppard PO, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sistrurus miliarius.
                                                                                                                                                                                                    WPI; 2002-269180/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                       molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                               14-AUG-2000;
15-AUG-2000;
15-AUG-2000;
20-DEC-2000;
                                 14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD32057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD32057
셤
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

DNA encoding novel human diagnostic protein #20714

13-FEB-2002

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New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
"CDS does not include start codon"
                              30..434
/*tag= c
/product= "Mature Zsnk4 protein"
                                                                                                                                                                                                                                                            Claim 5; Page 75; 79pp; English.
                                                                                                                     2000US-225087P.
2000US-225489P.
2000US-225490P.
                                                                                             13-AUG-2001; 2001WO-US25310
                                                                                                                                              2000US-356997P
                 3..29
/*tag= b
       /partial
                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                             Sheppard PO, Bishop PD;
 note=
                                                                                                                                                                                             WPI; 2002-269180/31.
P-PSDB; AAE20180.
                                                                                                                                                                                                                                                                                                                                                                                                     protein, Zsnk4 gene.
                                                                                                                                                                                                                                             molecular biology
                                                               WO200214364-A2
                                                                                                                              15-AUG-2000;
15-AUG-2000;
                                                                                                                                               20-DEC-2000;
                                                                                                             14-AUG-2000;
14-AUG-2000;
                sig peptide
                                mat_peptide
                                                                               21-FEB-2002
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

P-PSDB; ABG20723

(HYSE-) HYSEQ INC

30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

WO200175067-A2.

11-OCT-2001.

Claim 1; SEQ ID No 20714; 103pp; English.

biodiversity

The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide can be used as standards or as unknowns
protein chemistry and antibody production and analysis. The
polymucleotide or polypeptide are also useful in identifying
proteins by western blotting, protein purification, determining the
weight of expressed polypeptides as a ratio to total protein expressed,
identifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectrometry, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland

Sequence 580 BP; 154 A; 133 C; 163 G; 130 T; 0 other

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Length:
Matches:
Conservative:
Mismatches:
Indels:
         0.346
66.00
86.67%
53.33%
61.11%
                              Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                    Query Match:
          Pred. No.:
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x AAD32057 (1-580) US-09-938-114-4 (1-17)

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1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
              g
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AAS84910 standard; cDNA; 1062 BP AAS84910; AAS84910

RESULT 12

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags and intentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or constituting a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical inseging of sites expressing (II). (I) and (II) are useful in tracting the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and an especial and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and an expression or biological activity and an especial and activity and acceptances are assess biodiversity and acceptances are assess and as a constant and acceptances are assessively and activity and acceptances are assessively and polynucleotide and polynucleotide sequences are assessively and polynucleotides are assessively and accepta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1062 BP; 293 A; 242 C; 248 G; 279 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
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ID AAQ24977 standard; DNA; 5140 BP.
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64.29$
56.48$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.47
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
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US-09-938-114-4 (1-17) x AAQ24977 (1-5140)

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Soluble mannose receptor peptide; ss DNA; receptor binding; cancer cells; targeting; probe; drug delivery; cell marker; fusion molecule; AZT; ricin; pertussis; cholera toxin; liposome; therapeutic agent; diagnostic agent; opportunistic infections; immunocompromised patients; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5140 BP; 1598 A; 994 C; 1175 G; 1373 T; 0 other;
                                           soluble mannose receptor peptide.
                                                                                                                                                                                                                                                                                                Disclosure; page 21-27; 37pp; English
                                                                                                                     Location/Qualifiers
59..4429
/*tag= a
                                                                                                                                                                                                              (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                 91WO-US08320,
                                                                                                                                                                                                90US-0609915.
                             (first entry)
                     (updated)
                                                                                                                                                                                                                                            WPI; 1992-183410/22.
                                                                                                                                                                                                                                                    P-PSDB; AAR24033
                                                                                                                                                                                                                                                                                                                                                                                                                                                           lotion
                                                                                                                                                                                                                             Ezekowitz RAB;
                                           ONA encoding
                                                                                                                                                                                06-NOV-1991;
                                                                                                                                                                                               06-NOV-1990;
                                                                                                        Homo sapiens
                                                                                                                                                   W09207579-A1
                     25-MAR-2003
18-NOV-1992
                                                                                                                                                                  14-MAY-1992
       AAQ24977;
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The mannose receptor protein (MRP), or at least one carbohydrate recognition domain of it derived from an extracellular portion, can specifically bind pro- or eukaryotic pathogens, eg bacteria, fungior viruses, with exposed configurations of mannose, pacteria, fungior viruses, with exposed configurations of mannose, and cytoplasmic playcoprotein. The protein lacks the MRP transmembrane and cytoplasmic regions and is capable of specifically targeting cells expressing the specified proteins. The MRPs can also target cancer cells which have any exposed mannose residues resulting from aberrant glycosylation. The proteins can be used as probes for such cells, or as fusion molecules for delivery of specific molecules, eg AZT, ricin, pertussis or cholers toxins, or CD4 to fix complement, or as an in vivo marker for immune system cells. The hybrid molecules are esp. capable of causing an effector molecule to be targeted to a cell, eg a virus. WRP and antibodies raised to it are also useful as therapeutic or chighnest agents, eg for Leishmania proamastigotes, Pheumocystis carinii, Candida albicans, Microbacterium tuberculosis, HIV or influenza virus, the antibodies are also useful to purify the MRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The protein may be administered as a coating on a liposome, or as
Soluble extracellular recombinant mannose receptor protein fragments - target mannose expressing cells for treatment and diagnosis of infections, cancer, etc.
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Length: Matches: Conservative: Mismatches:

30.3 61.00 71.43% 64.29% 56.48%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores:

Pred. No.:

Indels: Gaps:

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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerlectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymelectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the product of the treating disorders of the treating diagnostics, forensics, gene mapping, identification of mutations and the production of the treating the production of mutations and the production of the treating the production of the production of mutations and the production of the p
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 other;
                                1142 TGTCCTAGTCAGTGGCCGTATGCCGGTCACTGTTACAAG 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to isolated polynucleotide (I) and
CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5457
                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #20717.
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 20717; 103pp; English.
                                                                                                                                                                         BP.
                                                                                                                                                                         AAS84913 standard; cDNA; 5457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABG20726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                 AAS84913;
                                                                                                                RESULT 14
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us-09-938-114-4.rng

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The invention relates to new pigmy rattlesnake (Sistrurus miliarius)

venom gland proteins, which affect blood coagulation and platelet
aggregation system. The polypeptides, which affect blood coagulation and
platelet aggregation system, are useful in therapy and diagnostics. The
polypeptides are also useful as an educational tool in laboratory
creatioal kits for courses related to genetics and molecular biology,
protein chemistry and antibody production and analysis. The
polynucleotide or polypeptide can be used as standards or as unknowns
for testing purposes. The polypeptides are also useful in identifying
proteins by western blotting, protein purification, determining the
creation of expressed polypeptides as a ratio to total protein expressed,
dentifying peptide cleavage sites, coupling amino and carboxyl terminal
tags, mass spectromatery, circular dichroism to determine conformation or
affinity chromatography columns to purify the protein, cloning or
sequencing. The present sequence is Sistrurus miliarius venom gland
creating the protein acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which affect blood coagulation and platelet aggregation system, useful in therapy and diagnostics, or as tools in the study of genetics or
                                                                                                                                                                                                                                                                                 Pigmy rattlesnake venom gland protein Zsnk4, degenerate nucleic acid.
                                                                                                                                                                                                                                                                                                                      Pigmy rattlesnake; venom gland protein; blood coagulation; therapy; platelet aggregation; ds.
                                                                                                     CysProSerdluTrpSerSerTyrGluGlyPheCysTyrLys 15
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   Indels:
Gaps:
                                             US-09-938-114-4 (1-17) x AAS84913 (1-5457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 76; 79pp; English.
                                                                                                                                                                                    AAD32058 standard; DNA; 432 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-225072P.
2000US-225087P.
2000US-225489P.
2000US-225490P.
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 56.48%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheppard PO, Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                     Sistrurus miliarius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-269180/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                   WO200214364-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
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20-DEC-2000;
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                                                                                                                                                                                                                  AAD32058;
Query Match:
DB:
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432

Conservative: Mismatches:

Length: Matches:

2.16 60.00 78.57% 50.00%

Best Local Similarity:

Percent Similarity:

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15, Appl 1, Appli 16, Appl 3, Appli 1, Appli 583, App 2, Appli 518210

25, Appl 30, Appl 1, Appl 19, Appl 19, Appl 10, Appl 10, Appl 11, Appl 14, Appl 8, Appl 15, Appl 14, Appl 1534, Ap 1534, Ap

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Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Sequence 42,
                                                                                                                      Sequence
                                                                                                                                                   Patent No.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hui-Ran Chen
TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM
VENOM OF AGKISTRODON ACUTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng, Jing Liu, Li-Wen Niu, Wan-Zhi Huang, Zhen-Yu Xu, Dan Luo, Lian-Di Kang, Jin-Guo Ding, Fang Rong, Yan Liu and
US-08-543-246B-5

US-09-016-434-1347

US-09-016-434-1347

US-08-543-246B-15

US-08-543-246B-15

US-08-517-605-16

US-08-517-605-16

US-08-517-605-16

US-08-517-605-16

US-09-194-415-13

US-09-194-612A-2

5182210-9

US-09-194-612A-2

5182210-9

US-09-194-612A-2

US-09-194-612A-2

US-09-489-847-51

US-08-432-6965A-30

US-09-489-847-51

US-09-489-847-51

US-09-613-566-19

US-09-613-246B-14

US-09-252-991A-1430

US-09-252-991A-1430

US-09-252-991A-1430

US-08-772-440-20

US-08-772-440-20
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US-08-743-168B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-111-470-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASTSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,740
FILING DATE: 10-Apr-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-058-740-12
; Sequence 12, Application US/09058740
; Patent No. 6489451
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Chen, Anthony C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/CQ21 1/USP3TO spool/US09938114/runat 08122003 091001 22878/app query.fasta_1.725
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-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_NIN=0 -ALIGN=15
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-USRE=LS09938114_@CGN 1 1_95_@runat_0812203 -931001 _22878 -NORD-6 -ICPU=3
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO MADP -LARGEQUERY -NEG SCORES=0 -MATRIX-DSPELOCK=100 -LONGLOG
-NO TIMBOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPORT=0.5 -FGAPOP=6
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Sequence 4, Appli
Sequence 3, Appli
Sequence 17, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 11, Appli
                                                                                         December 8, 2003, 13:49:04 ; Search time 13.4057 Seconds (without alignments) 559.725 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                            OM protein - nucleic search, using frame_plus_p2n model
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US-08-612-840A-7
US-09-585-228-1
US-08-543-246B-4
US-08-543-246B-7
US-08-543-246B-7
US-08-543-246B-12
US-08-543-246B-13
US-08-543-246B-13
US-08-543-246B-11
US-09-591-435-10
US-09-591-435-10
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                                                                                                                                                                                                                                                                                                   569978 seqs, 220691566 residues
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Maximum Match 1008
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match
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Database :

Result No.

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Pred. No.:
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APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TOBATIANTI YOUNGTOO, RYOTA
APPLICANT: YOSHIMOTO, RYOTA
APPLICANT: YOSHIMOTO, RYOTA
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence
LOCATION: 3...440
OTHER INFORMATION: "N" stands for any base.
"Xaa" stands for any amino acid.
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-938-114-4 (1-17) x US-09-058-740-12 (1-454)
REGISTRATION NUMBER: 38,673
REFERENCE/BOKER: 233/298
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0410
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1093
ATTORNEY/AGENT INFORMATION
NAME: NO. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Nacyuki
                                                                                                                                                                      LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUKUCHI, Naoyuki
YAMAMOTO, Hiroshi
NAGANO, Mitsuyo
                                                                                                                                                                                                                                                                                                                                                                                                                                            3.26e-08
101.00
94.12%
94.12%
                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       va
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                   US-09-058-740-12
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1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
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APPLICANT: Paddington, Christopher S.
APPLICANT: West, James W.
APPLICANT: West, James W.
APPLICANT: Holly, Richard N.
APPLICANT: Holly, Richard N.
TITLE OF INVENTION: FOUR-HELICAL BUNDLE PROTEIN ZSIG81
FILE REPERENCE: 99-13
CURRENT APPLICATION NUMBER: US/09/585,228
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: US 60/137,057
HARLIER OF FILING DATE: 1999-06-01
NUMBER: OF SEQ ID NOS: 36
SOFTWARE: FASHERO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                           690
112
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2
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-938-114-4 (1-17) x US-09-585-228-1 (1-1600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Crotalus horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-585-228-1; Sequence I. Application US/09585228; Patent No. 6531576; GENERAL INFORMATION:
                TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
                                                                                                                                                                                                                                                                                                                                                           5.53e-05
83.00
88.24%
70.59%
76.85%
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9
54.00
61.54%
53.85%
50.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (134)...(655)
NAME/KEY: sig_peptide
LOCATION: (134)...(184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                       LOCATION:
US-08-612-840A-7
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                                                                                                                                                                                                                                      STRAIN:
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DNA and amino acid sequence specific for natural killer cells
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APPLICATION NUMBER: US/08/543,246B
1420 TGCCCCAGCTCTTGGCACCATTATTCTGCTTTTTT 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION:
TELEPHONE: 908-522-6927
                                                                                                                                         APPLICANT:
TITLE OF INVENTION: DNA and amino acid seque:
TITLE OF INVENTION: natural killer cells
TITLE OF INVENTION: 24
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-938-114-4 (1-17) x US-08-543-246B-4 (1-360)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION NUMBER: CT/MS92/02469
FILING DATE: 27-MAR-1992
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                Sequence 4, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08543246B Patent No. 6262244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) ANYPOTHETICAL: NO ANTI-SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.00
61.54%
53.85%
48.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 360 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908-522-6955
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 07901-1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ercent Similarity:
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Pred. No.:
                                                             US-08-543-246B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-543-246B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
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GENERAL INFORMATION:

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DNA and amino acid sequence specific for natural killer cells
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CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     SOTTWARE: Perentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6927
TELEFEXX: 908-522-6955
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-938-114-4 (1-17) x US-08-543-246B-3 (1-405)
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Matches:
                                                                                                             ADDRESSE: Michael W. Glynn
ADDRESSE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
FILING DATE: 24-SEP-1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
APPLICANT:
TITLE OF INVENTION: DNA
TITLE OF INVENTION: nat.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO US-08-543-246B-3
                                                                                                                                                                                                                               as
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US-08-543-246B-7
                                                                                                                                                                                                                               COUNTRY:
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us-09-938-114-4.rni

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APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells
CORRESPONDENCE ADDRESS:
                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
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                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER:
US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1993
ATTORNEY AGENT INFORMATION:
NAME: KASSENOFF, MELVYN M.
REGISTRATION NUMBER: 26,389
REFERRATION NUMBER: 26,389
REFERRATION NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-54-246B-12
Sequence 12, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 564 Morris Avenue
Summit,
564 Morris Avenue
                                                                         ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.18
52.00
61.54%
53.85%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07901-1027
COMPUTER READABLE FORM:
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                  Summit,
NJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-543-246B-7
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                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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DB:
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CENTERLY ANTECONSTRUCTION:

APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE: Michael W. Glynn
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6582244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US

ZIP: CONTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 IGTCCTGAGGAGTGGATTACATATTCCAACAGTTGTTAC 339
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                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION NUMBER: US 07/676,663
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY,AGENT THOROMATION:
NAME: KASSENOFF, MALVON M.
REGISTRATION NUMBER: 26,389
REPRENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEPHONE: 908-522-6927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-938-114-4 (1-17) x US-08-543-246B-12 (1-645)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.00
61.54%
53.85%
48.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-543-246B-12
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us-09-938-114-4.rni

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TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 TGTCCTGAGGAGTGGATTACATATTCCAACAGTTGTTAT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
         FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27-MAR-1992
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NOMBER: 25,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: 908-522-6955
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
Mismatches:
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FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/543,246B FILING DATE:
US 07/676,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-543-246B-11; Sequence 11, Application US/08543246B; Patent No. 6262244; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: ...
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~MEDIUM TYPE: IBM PC compatible
~~MOTITER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 693 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.00
61.54%
53.85%
48.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-543-246B-13
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE
TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL
TITLE OF INVENTION: AND MEDICAL CONDITIONS
TITLE OF INVENTION: AND MEDICAL CONDITIONS
TITLE OF INVENTION: AND MEDICAL CONDITIONS
TITLE REPERENCE: GENO.200.2
CURRENT APPLICATION NUMBER: US/09/591,435
PRIOR FILING DATE: 2000-06-09
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,263
PRIOR APPLICATION NUMBER: 60/073,263
PRIOR APPLICATION NUMBER: 60/099,987
PRIOR PILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099,987
PRIOR PILING DATE: 1998-09-02
PRIOR SEQ ID NOS: 13
SOCTWARE: PATENTIN VOYE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 TGTCCTGAGGAGTGGATTACATATTCCAACAGTTGTTAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REPERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 908-522-6957
TELEFAX: 908-522-6957
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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Matches:
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Patent No. 6280953
GENERAL INFORMATION:
APPLICANT: MESSIER, WALTER
APPLICANT: SIKELA, JAMES M
                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.54%
53.85%
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53.85%
48.15%
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US-09-591-435-9
                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                             16.5
52.00
76.92%
53.85%
48.15%
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8..700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                      Percent Similarity:
Best Local Similarity:
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LOCATION: E

PEATURE:

NAME/KEY: II

LOCATION: E

UCS-10-543-246B-5
                                         Alignment Scores
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    JS-09-591-435-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                  Query Match:
                                                             Pred. No.:
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; Sequence 11, Application US/09591435
; Patent No. 6280953
; GENERAL INFORMATION:
    APPLICANT: MESSIER, WALTER
; APPLICANT: MESSIER, WALTER
; TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL
; TITLE OF INVENTION: AND MEDICAL CONDITIONS
; FILE REFRENCE: GENO. 200. 2
; CURRENT FILING DATE: 2000-06-09
; PRIOR PEPLICATION NUMBER: 09/591,435
; CURRENT FILING DATE: 1999-01-29
; PRIOR PELING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: 60/073,263
; PRIOR SECUIO NOWER: 60/073,263
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 13
                                                                                              Sequence 10, Application US/09591435
Sequence 10, Application US/09591435
Sequence 10, Ca80953
Sequence 10, Ca80953
Sequence No. 6280953
TEREN INFORMATION:
TITLE OF INVENTION: BEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL TITLE OF INVENTION: AND MEDICAL CONDITIONS
FILE REFERENCE: GENO. 200. 2
CURRENT FILING DATE: 2000-06-09
FRIOR PELLING DATE: 1090-06-09
PRIOR PELLING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 09/240,915
PRIOR APPLICATION NUMBER: 60/073,263
PRIOR PELLING DATE: 1998-01-30
PRIOR PELLING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE PATENTING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 10
LENGTH: 1212
CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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52.00
76.92%
53.85%
48.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Pan troglodytes
US-09-591-435-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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LENGTH: 1212
                                                                                   US-09-591-435-10
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APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for TITLE OF INVENTION: natural killer cells
TITLE OF INVENTION: 1.24
CORRESPONDENCE: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
                                                                                                                                                                                                                                                                766 TGCCCCTGGGAATGGACATTCTTCCAAGGAAACTGTTAC 804
                                                                                                                                                                                                                                  2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                  US-09-938-114-4 (1-17) x US-09-591-435-11 (1-1212)
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APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRICK APPLICATION NUMBER: BCT/US92/02469
FILING DATE: 27-MAR-1992
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFRENCE/DOCKET NUMBER: 118-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6957
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
```

```
GENERAL INFORMATION:

APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCES: 1490
CORRESPONDENCES: NCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
THEWITH
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                        356 TGTCCTGAGGAGTGGATTACATATTCCAACAGTTGTTAT 394
                                                                                                                                                                                 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                          US-09-938-114-4 (1-17) x US-08-543-246B-5 (1-1222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REFERENCE/DOCKET NUMBER: 37,071

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRAX: (650) 845-055

TELEPRAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1347:

SEQUENCE CHARACTERISTICS:
                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                           Sequence 1347, Application US/09016434
Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1223 base pairs
                 16.7
52.00
61.54%
53.85%
48.15%
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61.54%
53.85%
48.15%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: GENBANK
CLONE: 935060
US-09-016-434-1347
                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                               US-09-016-434-1347
Alignment Scores:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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US-09-938-114-4 (1-17) x US-09-016-434-1347 (1-1223)

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APPLICANT: Littuan, Dan R.
APPLICANT: Littuan, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Won, Douglas S.
APPLICANT: Won, Douglas S.
APPLICANT: Geijtenbeck, Tree
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT APPLICATION NOS: 17
SOFTWARE: PATENTIN VET. 2.00
                         356 TGTCCTGAGGAGTGGATTACATATTCCAACAGTTGTTAT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807 IGICCCTGGGAATGGACATTCTTCCAAGGAAACTGTTAC 845
        14
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2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: December 8, 2003, 17:27:05 Job time : 15.4057 secs
                                                                                                                     ; Sequence 1, Application US/09517605; Patent No. 6391567; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3
52.00
76.92%
53.85%
48.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (42)..(1253)
US-09-517-605-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 1312
                                                                                                    US-09-517-605-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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Run on:

Sequence:

Sequence 1, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli

94, Appl 94, Appl 9, Appli 9, Appli

Sequence 94, Sequence 94,

sequence 37, Appl Sequence 37, Appl Sequence 230, App

Sequence 37 Sequence

Sequence 230,

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

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APPLICANT: KAYAHARA, TAKASHI
APPLICANT: KAYAHARA, TAKASHI
APPLICANT: FUTAKI, FUMIE
APPLICANT: SIZUKI, ELICHIRO
APPLICANT: GONDOH, KEIKO
APPLICANT: GHENA, MOBUHISA
APPLICANT: SHIMBA, MOBUHISA
APPLICANT: SHIMBA, MOBUHISA
APPLICANT: SHIMBA, MOBUHISA
APPLICANT: SHIMBA, MOBUHISA
APPLICANT: ANADA, NAOYUKI
TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING THE FILE REFRENCE: 214760USO
CURRENT PILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALENTIN Version 3:1
SEQ ID NO 2
LENGTH: 690
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09969763
Publication No. US20020198363A1
GENERAL INFORMATION:
    KITO, MORIKAZU
KAYAHARA, TAKASHI
FUTAKI, FUMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FUKUCHI, NAOYUKI APPLICANT: KITO, MORIKAZU
  7477229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-969-763-2
   Command line parameters:

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-Q=(GGD2_1/USPTO_SPOOl/US09938114/runat_08122003_091002_22963/app_query.fasta_1.725
-DB=Published_Applications_Na_-QFMT=fastap_SUFFIX=rnpb_-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITG=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_NN=0 -ALIGN=15. -MODE=LOCAL_OUTPMT=ptto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -USRR=US09938114_@CGN_11_S04_@runat_08122003_091002_22963
-NORU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NOS_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG -DEV_TIMEOŪT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE=6 -DELDEXT=7
                                                                   December 8, 2003, 16:08:50; Search time 67.6114 Seconds (without alignments) 835.675 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1. /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/PCTNEW PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/PCTNEW PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5. /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
6. /cgn2_6/ptodata/2/pubpna/PCTUG_PUBCOMB.seq:*
7. /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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14. /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
15. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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17. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
18. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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11. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
18. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
19. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
19. /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                   - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        2201672 seqs, 1661799599 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                     1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                 US-09-938-114-4
108
                                                                                                                                                           BLOSUM62
                                                                                                                Title:
Perfect score:
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Jatabase :

Description

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Query Match Length DB

Score

Result

Sequence

Seguence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence

Sequence

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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 1, Application US/10226420
; Publication No. US20330157686A1
; GENERAL INFORMATION:
; APPLICANT: Shappard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-7
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT PILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09929230

Patent No. US20020161203A1

GENERAL INPORMATION:

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION:

FILE REFERENCE: 00-72

CURRENT APPLICATION NUMBER: US/09/929,230

CURRENT APPLICATION NUMBER: US/09/929,230

CURRENT FILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FASESQ for Windows Version 4.0
                                                                                                                             690
122
22
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12
2
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                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                  US-09-938-114-4 (1-17) x US-09-969-763-2 (1-690)
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78.00
82.35%
70.59%
72.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Sistrurus miliarius
                                                                                                                                 7.15e-05
TYPE: DNA ORGANISM: Crotalus harridus FEATURE:
                                                                                                                                             83.00
88.24%
70.59%
76.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: CDS
; LOCATION: (3)...(455)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ZSHK2
US-09-929-230-1
                                       NAME/KEY: CDS
LOCATION: (66)..(512)
CTHER INFORMATION:
US-09-969-763-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 483
                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-929-230-1
                                                                                                                                                                                       Query Match:
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160 GATTGTCCCTCTGGTTGGTCCTCCTATGATCAGCATTGCTACAGGGTCTTC 210
                                                                                                                                                                                                                                                                                                                                                                                                               60 GATTGTCCCTCTGACTGGTCCTCCTATGATCAGCATTGCTACAAGGTCTTC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                                                                                                                                                                                                                                                1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-929-230-4
US-09-929-230
Sequence 4, Application US/09929230
Patent No. US-20020161203A1
GENERAL INFORMATION:
TITLE REPRESENCE: 00-72
TITLE REPRESENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRASESO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721
11
2
4
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                US-09-938-114-4 (1-17) x US-10-226-420-1 (1-483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10226420; Publication No. US20030157686A1; GENERAL INFORMATION: APPLICANT: Sheppard, Paul O.
SEQ ID NO 1
LENGTH: 483
TYPE: DNA
ORGANISM: Sistrurus miliarius
FEATURE:
NAME/KEY: CDS
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (0) ... (0)
OTHER INFORMATION: ZsnK2
US-10-226-420-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Sistrurus miliarius
                                                                                                                                                                                                                                            0.000342
                                                                                                                                                                                                                                                          78.00
82.35$
70.59$
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76.47%
64.71%
65.74%
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US-09-929-230-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (91)...(546)
NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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LENGTH: 721
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATLESNAKE VENOM GLAND PROTEINS
FILE REPERENCE: 00-72
CURRENT APPLICATION NUMBER: US/10/226,420
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
IENGTH: 721
TYPE: DNA
ORGANISM: Sistrurus miliarius
FRATURE:
NAMM-KEY: CDS
LOCATION: (91)...(546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09929230
Patent No. US20020161203A1
Patent No. US20020161203A1
FAPPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TILLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT APPLICATION NUMBER: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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                                                                                                                                                                                                                                                                                                                             0.00873
71.00
76.47%
64.71%
65.74%
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66.00
64.71%
52.94%
61.11%
                                                                                                                                                                                                                                NAME/KEY: misc feature
| LOCATION: (0) ... (0)
| OTHER INFORMATION: Zsnk3
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Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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Pred. No.:
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LENGTH: 453
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US-09-929-230-3
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NAME/KEY: misc_feature
LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393,
LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRATURE:
NAME/KEX: misc_feature
LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
LOCATION: 168, 171, 174, 180, 189, 192, 204, 210, 213, 219, 222,
LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
                                                                                             58 GAYTGYCCNWSNGAYTGGWSNWSNTAYGAYCARCAYTGYTAYAARGTNTTY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GAYTGYCCNWSNGAYTGGWSNWSNTAYGAYCARCAYTGYTAYAARGTNTTY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                           1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
                                                                                                                                                                                                                             Sequence 3, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sishop. Paul O.
; TITLE REFERENCE: 00-72
; CURRENT APPLICATION RATTLESNAKE VENOM GLAND PROTEINS
; FLIE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09929230
PREENT NO. US20020161203A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
APPLICANT: Bishop, Paul D.
APPLICANT: SISHOP, Paul D.
FITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REPERENCE: 00-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
US-09-938-114-4 (1-17) x US-09-929-230-3 (1-453)
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Matches:
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CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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61.11%
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Best Local Similarity:
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LENGTH: 453
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PatentIn version 3.1
NUMBER OF SEQ ID NOS: 166
                                                               TYPE: DNA

REATURE:
REATURE:
LOCATION:
LOCATION:
COTHER INFORMATION:
US-09-870-759-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (104)..(4474)
; OTHER INFORMATION:
US-09-751-708A-94
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LENGTH: 5185
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
              SOFTWARE: Paten
SEQ ID NO 94
LENGTH: 5185
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Sequence 94, Application US/09870759

Sequence 94, Application US/09870759

Sequence 920220177551A1

Sequence 94, Application US/09870759

PERERAL INFORMATION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US 60/208,128

PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 GATTGTCCCTCTGTGATTGGTATGCCTATGATCAGTATTGCTACAGG 80
                                                                                                                                                                                                                                                                                         1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
                                                                                                                                                                                                                                                                                                                  36 GATTGTCCCTCTGATTGGTATGCCTATGATCAGTATTGCTACAGG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
                                                                                                                                                                                                                                                                                                                                                                            WS-10-226-420-7
Sequence 7, Application US/10226420
Publication No. US20030157686A1
GENERAL INFORMATION:
APPLICANT: Bishop, Paul D.
TITLE REPRENCE: 00-72
CURRENT PLINGN: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT PILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Migmatches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                            US-09-938-114-4 (1-17) x US-09-929-230-7 (1-580)
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86.67%
53.33%
61.11%
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86.67%
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                LOCATION: (3)...(434)
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Zsnk4
US-09-929-230-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
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LOCATION: (3)...(434)
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Query Match:
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Best Local Similarity:
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   NAME/KEY: CDS
                                                                                                                        Alignment Scores:
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                                                                                                                                          Pred. No.:
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us-09-938-114-4.rnpb

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Best Local Similarity:
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US-10-125-540-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 37
LENGTH: 618
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                                    Query Match:
DB:
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                                                                                                                                                                                            OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.

NAME/KEY: misc feature.
LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 111, 10CATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180, LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276, LOCATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360

OTHER INFORMATION: n = A,T,C or G

NAME/KEY: misc feature
LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: This degenerate nucleotide sequence encodes the OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.

FRATURE:
NAME/KEY: misc feature
LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180, LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180, LOCATION: 117, 284, 297, 300, 315, 327, 330, 345, 348, 360
OTHER INFORMATION: n = A,T,C or G
LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-226-420-9

Sequence 9, Application US/10226420

Publication No. US20030157686A1

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS

FILE REFERENCE: 00-72

CURRENT APPLICATION NUMBER: US/110/226,420

CURRENT FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 9

LENGTH: 432
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/09/929,230 CURRENT FILING DATE: 2001-08-13 NUMBER OF SEQ ID NOS: 14 SOUTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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60.00
78.57%
50.00%
55.56%
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Best Local Similarity:
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Pred. No.:
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DB:
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Sequence 37, Application US/09764870

Batent No. US20020042386A1

Batent No. US20020042386A1

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE REFERENCE: PT214

CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 646

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.

TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DAIE: 2002-04-19
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
                                                                                                         1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
                                                                                                                            618
8 2
3 3
0 0
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   m 0 0
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 Mismatches:
Indels:
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Indels:
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                                                                    US-09-938-114-4 (1-17) x US-10-226-420-9 (1-432)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (65)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (598)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (556)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37, Application US/10125540 Publication No. US20030059875A1 GENERAL INFORMATION:
50.00%
55.56%
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.26
58.00
76.92%
61.54%
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
```

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CREATURE:

NAME/KEY: misc_feature

LOCATION: (48)

COTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature

LOCATION: (65)

OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature

LOCATION: (556)

OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature

LOCATION: (588)

COTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature

LOCATION: (588)

COTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature

LOCATION: (588)

COTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature

LOCATION: (588)

COTHER INFORMATION: n equals a,t,g, or c
US-10-125-540-37
LENGTH: 618
TYPE: DNA
ORGANISM: Homo sapiens
```

US-09-938-114-4 (1-17) x US-10-125-540-37 (1-618)

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1.26 58.00 76.92% 61.54% 53.70%

Percent Similarity:
Best Local Similarity: (Query Match:

Alignment Scores: Pred. No.: Score:

Search completed: December 8, 2003, 19:36:07 Job time : 69.6114 secs

us-09-938-114-4.rnpb

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

December 8, 2003, 09:49:54; Search time 3.4 Seconds (without alignments) 480.843 Million cell updates/sec

108 1 DCPSEWSSYEGFCYKPF 17 US-09-938-114-4 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		-H	aqkisacutacin beta	coadulation factor		aggretin beta chai	factor TX/factor X	tokaracetin alnha	factor IX/factor X	botrocetin alpha c	C	alboadgredin-B bet		coagulation factor		Coagulation factor	alboaddredin-R aln		π	alpha	multactivase (EC 3	ot o	bothrojaracin - ja	عي ا	5	1	mannose receptor n	lectin SPI-2 Cast	12 E E E		hypothetical prote
			C7135	C4691	C4329	C7105	088	156006	53088	A47267	B47267	A56829	JC7134	JC4690	556007	B42972	B56829	JC2415	JC5059	JC5058	PC4421	A36563	A48630	\$55679	TL	S29855	A48925	PX0080	A38609	A39086	600
		8	JC7	JC4	JC4	JC7	B53	S 26	A53	A47	B47	A56	JC7	JC4	856	B42	B56	JC2	JCS	JCS	PC4	A36	A48	S 55	LNRTL	\$29	A48	PX0	A38	A39	D71
		BB :				(7)	~	7	N	7	ď	7	N	7	N	N	~	7	7	7	7	Н	~	ď	Н	N	Н	~	7	Н	7
		Match Length	146	146	129	146	30	40	30	133	125	40	152	152	40	123	40	123	125	131	29	1456	16	71	284	284	1455	46	135	2415	143
de	Query	Match	93.5	7.06	87.0	87.0	77.8	75.9	75.0	75.0	73.1	71.3	71.3	70.4	69.4	65.7	63.9	62.0	59.3	59.3	57.4	56.5	53.7	53.7	50.9	50.9	50.9	50.0	50.0	50.0	49.1
		Score	101	98	94	94	84	82	81	81	79	77	77	92	75	71	69	67	64	64	62	61	58	58	52	52	52	54	54	54	
	Result	No.	-	7	e	4	2	9	7	80	σn	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Coagulation factor IX/factor X-binding protein chain A precursor - habu C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4661; B39332; JC4330
R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem. Biophys. Res. Commun. 220, 387-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from sr A;Reference number: JC4699; MUID:96184662; PMID:8645314
A;Reference number: JC4691
A;Rolecule 'Ype: mRNA
A;Residues: 1-146 cART:
A;Cross-references: DDBU:D8332; NID:g1402641; PIDN:BAM1888.1; PID:g1402642

RiAtoda, H.; Hyuga, M.; Morita, T. J. Biol. Chem. 266, 14903-14911, 1991 A:Title: The primary structure of coagulation factor IX/factor X-binding protein isolated otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.

lectin. galactose/
JX0209
~
304
49.1
53 49.1

ALIGNMENTS

RESULT 1 JC7135	
agkisacutacin beta chain precursor - sharp-nosed viper N;Alternate names: fibrinogenlytic venom protein	Ы
C:Species: Agkistrodon acutus (sharp-nosed viper)	000 to 00
C; Accession: JC7135; PC7038 R: Cheng, X : Oian, V : Iiii, O : Ii B v v : Zhang, M	
Biochem. Biophys. Res. Commun. 265, 530-535, 1999	; Liu, J.
A,Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom A,Reference number: JC7134: MUID:20025479: PMTD:10558903	ning of a new fibrinogenlytic ven-
A, Accession: JC7135	1
A;Molecule type: mRNA A;Residues: 1-146 <che></che>	
A; Cross-references: GB: AF176421	
A; Experimental source: venom gland	
A; Molecule type: protein	
A;Residues: 24-50;59-83;102-107;112-114 <ch2></ch2>	
C;Superfamily: tetranectin; C-type lectin homology C;Keywords: disulfide bond: heterodimer: venom	
F:1-23/Domain: signal sequence #status predicted <sig> F:24-146/Product: agkisamisarin heta chain #status ganazimental warm.</sig>	Washington (extraoring of the contract of the
Chery March	retimental suri
Similarity 94.1%; Pred. No. 4.1e-07.6; Conservative 0: Mismatched	; Length 146; 7; Thdele n. Cans n.
1 DCPSEWSSYEGFCYKPF 17	2000
Db 24 DCPSEWSSYEGHCYKPF 40	
RESULT 2	

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C;Accession: B53088
R;Sekiya, F.; Atoda, H.; Morita, T.
Biochemistry 32, 6892-6897, 1993
A;Title: Isolation and characterization of an anticoagulant protein homologous to botroc A;Reference number: A53088; MUID:93326575; PMID:8334120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tokaracetin alpha chain - Trimeresurus tokarensis (fragment)
N.Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Accession: S56006
R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai
Biochem, J. 308, 947-953, 1995
A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib a
A;Reference number: S56006; MUID:97104297; PMID:8948455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Sekiya, F.; Atoda, H.; Morita, T.
Biochemistry 32, 6892-6897, 1993
A;Title: Isolation and characterization of an anticoagulant protein homologous to botroc
A;Reference number: A53088; MUID:93326575; PMID:8334120
                                                                                                                                                                                                                                                                                                                                                                                      factor IX/factor X-binding anticoagulant protein A chain - jararaca (fragment)
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C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: A53088
                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bothrops jararaca (jararaca)
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
                                   Gaps
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Pred. No. 6.5e-05;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 84; DB 2; Length 30; llarity 76.5%; Pred. No. 2.7e-05; Conservative 1; Mismatches 3; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: venom
A, Note: sequence extracted from NCBI backbone (NCBIP:135336)
   88.2%; Pred. No. 3.9e-06;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: tetranectin; C-type lectin homology
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                                                                                                                   1 DCPSEWSSYEGFCYKPF
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Best Local Similarity 70.6
Matches 12; Conservative
                                           Conservative
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A;Molecule type: protein
A;Residues: 1-30 <SEK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-30 <SEX>
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coagulation factor IX-binding protein A chain - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Accession: UC4329
B;Atcasion: UC4329
B;Atcasion: UC4329
J: Biochem. 118, 965-973, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav
A;Reference number: UC4329; MUID:96318509; PMID:8749314
A;Reference number: Drotein
A;Residues: 1-129 cATO>
C;Comment: This protein binds calcium.
C;Superfamily: tetranectin; C-type lectin homology
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; calcium binding; venom
F;2-137/Domain: C-type lectin homology cLCh->
F;2-137/Domain: C-type lectin homology sLCH->
F;2-137/Domain: C-type lectin hom
                                                                                                                                                                                                                           A,Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav A;Reference number: UC4329; MUID:96318509; PMID:8749314
A;Reference number: UC4329; MUID:96318509; PMID:8749314
A;Resence number: UC4330
A;Rolecule type: protein
A;Residues: 24-146 cAT2>
C;Superfamily: tetranecrin; C-type lectin homology
C;Superfamily: Letranecrin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; lectin; venom
F;1-23/Domain: signal sequence #status predicted cSIG>
F;24-146/Product: factor IX/X binding protein chain B #status predicted cMAT>
F;25-142/Domain: C-type lectin homology cLCH3
F;25-36,53-142/Domain: C-type lectin homology cLCH3
F;25-36,53-142/ID9-134/Disulfide bonds: #status predicted
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aggretin beta chain - Malayan pit viper

c;Species Calloselama rhodostoma (Malayan pit viper)

c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000

c;Accession: JC7105

R;Chung, C.H.; Au, L.C.; Huang, T.F.

Biochem. Biophys. Res. Commun. 263, 723-727, 1999

A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet

A;Reference number: PC7027; MUID:99443731; PMID:10512747

A;Accession: JC7105

A;Residues: 1-146 <CHU>

A;Residues: 1-146 <CHU>

C;Superfamily: tetranectin, C-type lectin homology

C;Superfamily: tetranectin, C-type lectin homology

C;Superfamily: tetranectin, C-type lectin yenom
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0
                                       A;Accession: B39332
A;Molecule type: protein
A;Residues: 24-146 <ATO.
R;Atoda, H.; Ishikam, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Blochem. 118, 965-973, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.0%; Score 94; DB 2; Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.7%; Score 98; DB 2; Length 146; 88.2%; Pred. No. 1.1e-06; ive 1; Mismatches 1; Indels
       number: A39332; MUID:91332000; PMID:1831197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DCPSEWSSYEGFCYKPF 17
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Matches 15; Conserv
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nes 15; Conserv
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N'Alternate names: fibrinogenlytic venom protein (Species: Agkistrodon acutus (sharp-nosed viper) (Cispecies: Agkistrodon acutus (sharp-nosed viper) (Cipate: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000 (Cipate: 04-Mar-2000 #text_change 24-Oct-2000 (Cipate: 04-Mar-2000 #text_change 24-Oct-2000 (Cipate: Name of Cipate: Name of
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A; Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous A; Reference number: A56829; MUID:93221514; PMID:8466514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alboaggregin-B beta chain - green pit viper (fragment)
C;Species: Trimeresurus albolabris (green pit viper)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
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                                                                        C, Superfamily: terranectin; C-type lectin homology
C; Superfamily: terranectin; heterodimer; venom
F;2-121/Domain: C-type lectin homology <LGN
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental
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                                             C; Complex: heterodimer of alpha (see PIR: A47267) and beta chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 152;
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                                                                                                                                                                                                                                                                                                                                        Score 79; DB 2; Length 125
Pred. No. 0.00043;
2; Mismatches 3; Indels
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Pred. No. 0.00032;
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A; Residues: 24-55; 34-86; 94-10; 94; 125-136; 137-152 CCH2:
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; heterodimer; venom
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Best Local Similarity 70.6%;
Matches 12; Conservative
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A;Experimental source: venom
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A; Residues: 1-152 < CHE>
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A;Status: preliminary
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A; Mesidues: 1-133 <USA>
A; Residues: 1-133 <USA>
A; Experimental source: venom
A; Note: sequence extracted from NCBI backbone (NCBIP:124085)
B; Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sugabochemistry 30, 1957-1964, 1991
A; Title: Isolation and chemical characterization of two structurally and functionally di
A; Reference number: A37958; MUID:91129280; PMID:1993206
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C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
C;Accession: B47267; C37958
B;Usami, Y: Fujimura, Y: Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator put A;Reference number: A47267; MUID:93157385; PMID:8430107
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A.Experimental Source: venom
A.Note: Sequence extracted from NCBI backbone (NCBIP:124086)
R.Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sl
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally A;Reference number: A37958; MUID:91129280; PMID:1993206
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C'Species: Bothrops jararaca (jararaca)
C'Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C'Baccession: A47267; B37958
R'Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 938-932, 1939
A;Title: Primary structure of two-chain borrocetin, a von Willebrand factor modulator A;Reference number: A47267; MUID:93157385; PMID:8430107
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A;Residues: 1-40 < EUJ>
C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Complex: heterodimer of alpha end beta (see PIR:B47267) chains
C;Superfamily: tetranectin; C-type lectin homology
C;Seywords: hemagglutinin; heterodimer; venom
F;2-128/Domain: C-type lectin homology <LCH>
F;2-128/Domain: C-type lectin homology <LCH>
F;2-13,30-128,103-120/Disulfide bonds: #stetus experimental
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Pred. No. 0.00024;
                                                                                                                               Query Match 75.0%; Score 81; DB 2; Length 30; Best Local Similarity 70.6%; Pred. No. 7e-05; Matches 12; Conservative 2; Mismatches 3; Indels
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:135337)
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C;Accession: B56829
R;Yoshida, E.; Pujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.; & Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993
A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous & A;Reference number: A56829; MUID:93221514; PMID:8466514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alboaggregin-B alpha chain - green pit viper (fragment)
C;Species: Trimeresurus albolabris (green pit viper)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                           A; Experimental source: venom
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Best Local Similarity
9; Conserva
                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <TAK>
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A;Molecule type: protein
A;Residues: 1-40 <YOS>
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Lokracetin beta chain - Trimeresurus tokarensis (fragment)

Lokracetin beta chain - Trimeresurus tokarensis (fragment)

N.Alternate names: platelet aggregation inhibitor; platelet antagonist

C;Species: Trimeresurus tokarensis

C;Species: Trimeresurus tokarensis

C;Accession: S56007

R;Kawasaki, T; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai

B;Kochem. J. 308, 947-953, 1995

A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib a

A;Title: Tokaracetin, S56006; MuID:97104297; PMID:8948455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiAtoda, H.; Hyuga, M.; Morita, T.
Di Biol. Chem. 266, 14903-14911, 1991
A; Hiel: The primary structure of coagulation factor IX/factor X-binding protein isolate
otein, terranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
                                                                                                                                                                      Coagulation factor IX/factor X-binding protein chain A precursor - habu

C;Species: Trimeresurus flavoviridis (habu)

C;Species: Trimerequence_revision 16-Aug-1996 #text_change 20-Jun-2000

C;Accession: JC4690; A39332

R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Biochem. Biophys. Res. Commun. 220, 382-387, 1996

A;Title: cDNA cloring of IX/X-BP, a heterogeneous two-chain anticoagulant protein from A;Reference number: JC4690; MUID:96184662; PMID:8645314

A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation factor X activating enzyme (BC 3.4.24.-) light chain - Russell's viper C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
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A, Residues: 24-152 4700-
B, Residues: 24-152 4700-
C; Superfamily: tetranectin; C-type lectin homology
C; Reywords: anticoagulant; blood coagulation; glycoprotein; hemolymph; lectin
E;1-23/Domain: signal sequence #status predicted <SIG>
E;24-152/Product: factor IX/X binding protein chain A #status predicted <MAT>
F;25-150/Domain: C-type lectin homology <LGH>
F;25-36,53-150,125-142/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-152 <MAT1>
A;Cross-references: DDBJ:D83331; NID:g1402639; PIDN:BAA11887.1; PID:g1402640
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24 DCSSGWSSYEGHCYKVF 40
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Best Local Similarity 64.79
Watches 11; Conservative
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A;Molecule type: protein
A;Residues: 1-40 <KAW>
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Matches 13; Conserv
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R.Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S. J. Biol. Chem. 267, 14109-14117, 1992
A.Fittle: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A nov A.Reference number: A42972; MUID:92332516; PMID:1629211
A.Contents: V. r. siamensis
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                                                                                                                                                                                                                                                                                                                                                                                                            A,Note: sequence extracted from NCBI backbone (NCBIP:108408) C;Superfamily: tetranectin, C-type lectin homology C;Keywords: hydrolase; metalloproteinase; venom; zinc F;4-121/Domain: C-type lectin homology <LCH>F;4-121,50anain: C-type lectin homology <LCH>F;4-15,32-121,98-113/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 65.7%; Score 71; DB 2; Le:
Best Local Similarity 70.6%; Pred. No. 0.0056;
Matches 12; Conservative 0; Mismatches 5;
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A; Note: sequence extracted from NCBI backbone (NCBIP:128751) C;Superfamily: tetranectin; C-type lectin homology C;Keywords: disulfide bond; heterodimer 63.9%; Score 69; DB 2; Length 40; 60.0%; Pred. No. 0.0042; tive 5; Mismatches 1; Indels Length 40;

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Gaps

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8, 2003, 09:55:35

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15.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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OM protein - protein search, using sw model

December 8, 2003, 09:46:14 ; Search time 2.23429 Seconds (without alignments) 357.812 Million cell updates/sec Run on:

US-09-938-114-4 Title: Perfect score:

1 DCPSEWSSYEGFCYKPF 17 Sequence:

BLOSUM62 Scoring table:

127863 seqs, 47026705 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P23807 trimeresuru	609		80	bothrops	6 trimeresu	P81113 trimeresuru		_	P23806 trimeresuru	7	P81397 agkistrodon		و	agkist		8 echis	homo s	6 crot	_	5 ratt	~	N	P49300 mus musculu	m	Q95mil pan troglod	7 home	Q9mzk6 macaca mula	P26715 homo sapien	O9mzj3 macaca mula	'n	4 homo	Q95mi4 pan troglod
SOMETHINE		ID	IXB TRIFL	снвв сконо	ABA4_TRIAB	CHBA_CROHO	BOTA_BOTJA	ABBB_TRIAB	ABA3_TRIAB	BOTB_BOTJA	ABA1_TRIAB	IXA_TRIFL	CVXB_CRODU	RHCA_AGKRH	ABBA_TRIAB	ECHB ECHCA	RHCB_AGKRH	ECHA ECHCA	MULR ECHML	MANR HUMAN	CVXA CRODU	LECH_MOUSE	LECH RAT	LECG CROAT	PGCA_HUMAN	MMGL_MOUSE	NKGF_HUMAN	NKGF PANTR	NKGC_HUMAN	NKGC MACMU	NKGA HUMAN	NKGA MACMU		NKGE_HUMAN	NKGE_PANTR
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æ		Match	7.06	9	ę.	9	L)	74.1	74.1	73.1	73.1	70.4	æ	9	m	N	σ	σ	~	9	н	0	50.9	0	0	49.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.⊥
		Score	86	86	86	83	81	80	80	79	79	16	74	72	69	67	64	64	62	61	26	52	55	54	54	53	52	25	52	52	. 52	52	25	201	22
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EMBL; D83332; BAA11888.1; -. PIR; JC4691; JC4691.

P81112 trimeresuru	P21063 vaccinia vi P24765 vaccinia vi	P49301 rattus norv	P98154 mus musculu	Q61361 mus musculu	Q28062 bos taurus	P14370 fowlpox vir	P07897 rattus norv	O61282 mus musculu	P13608 bos taurus	Q01758 osmerus mor
ABA2_TRIAB	VA40_VACCU	MMGL_RAT	IDD MOUSE	PGCB MOUSE	PGCB BOVIN	VOOS FOWPV	PGCA_RAT	PGCA MOUSE	PGCA BOVIN	ANP_OSMMO
4		П	Н	Н	Н	ч	٦	П	Н	н
134	168	306	548	883	912	167	2124	2132	2364	175
47.2	47.2	47.2	47.2	47.2	47.2	46.3	46.3	46.3	46.3	45.4
51	21	51	51	21	51	20	20	20	20	49
34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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MEDLINE=97331317; PubMed=9187649; Mizuno H., Atoda H., Morita T.; Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; Mizucture of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains.";

Nat. Struct. Biol. 4:438-441(1997).

-! FUNCTION: ANTICOAGULANT PROFIEM WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.

-! SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.

-! SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                            MEDLINE=96184662; PubMed=8645314; Matenzaki R., Atoda H., Morita T.; Matenzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.; "CDMA cloning of IX/A-BP, a heterogeneous two-chain anticoagulant protein from snake venom."
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                      IXB_TRIFL
PR3807; Q91247;
01-00V-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 220:382-387(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom;
MEDLINE=91332000; PubMed=1831197;
                                                                                                                                                                          Trimeresurus flavoviridis (Habu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atoda H., Hyuga M., Morita T.;
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RESULT 1
IXB_TRIFL
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Gaps

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2; Indels

Length 117;

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BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
           -i- SIMILARITY: Contains 1 C-type lectin family domain. SMART; SWO0034; CLECT; 1. PROSITE; PSSO015; C_TYPE_LECTIN 1; 1. PROSITE; PSSO041; C_TYPE_LECTIN_2; 1.
                                                                                                                               SIMILARITY.
07835BBCB61E9EAD CRC64;
                                                                                                                                                                 79.6%; Score 86; DB 1; 76.5%; Pred. No. 8e-06; live 2; Mismatches
                                                                       C-TYPE LECTIN
                                                                                                                    (POTENTIAL)
-!- SUBCELLULAR LOCATION: Secreted.
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76.58;
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nes 13; Conservative
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117 AA;
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13;
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P811<u>1</u>4;
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                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lectin.
DOMAIN
                                                              ectin.
                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          datches
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                            RESULT 3
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  SHAFFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=96420502; PubMed=8823201; Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M., Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M., Smith A.I., Lopez J.A., Berndt M.C.; Binding of a novel 50-kilodalton alboaggregin from Trimeresurus albolabris and related viper venom proteins to the platelet membrane glycoprotein ID-IX-V complex. Effect on platelet aggregation and glycoprotein Ib-mediated platelet activation.", Biochemistry 35:12629-12639(1996).

-- FWOTION: Binds to platelet GPIB/IX receptor system, inhibits VWF binding, and stimulates agglutination.

-- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                           COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
CHH-B beta subunit.
Crotalus horridus horridus (Timber rattlesnake).
Crotalus horridus chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Crotalus.
                                                                                                                               C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SINILARITY.

BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               90.7%; Score 98; DB 1; Length 146; 88.2%; Pred. No. 1.8e-07; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA
            PDB; 1BJ3; 16-AUG-99.
InterPro; 1PR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SNART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCPSDWSSYEGHCYKPF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue=venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CROHO
                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                DISULFID
                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                               STRAND
                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P81509;
                                                                                                                                                                                                                                                                              STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
CHBB_CROHO
                                                                                                             CHAIN
                                                                                                                                                                                             TURN
                                                                                                                                                                                                                                                       TURN
                                                                                                                                                                                                                                                                    TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                               Trimeresurus albolabris (White-lipped pit viper).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=98189535; PubMed=9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Kozlycte J.J., Niewiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 86; DB 1; Length 123
Pred. No. 8.4e-06;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23807; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; D4CFBEE1219C9B1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN (LONG FORM)
                                                                    15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 4.
123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00235; Antifreezell.
InterPro; IPR001304; Lectin_C.
Pfam; PR00059; lectin_c; 1.
PRINTS; PR00356; ANTIFREZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DCPSDWSSYEGHCYRVF 17
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Sci. U.S.A. 90:928-932(1993).

us-09-938-114-4.rsp

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Proc. Natl. Acad.
                  SEQUENCE OF 1-40.
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                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABBB_TRIAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                            MEDLINE=96420502; PubMed=8823201;
Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M., Smith A.I., Lopez J.A., Berndt M.C.;
"Binding of a novel 50-kilodalton alboaggregin from Trimeresurus
                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH C-92 IN BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93157385; PubMed=8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                  76.9%; Score 83; DB 1; Length 127; 70.6%; Pred. No. 2.3e-05; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                        -!- SUBUNIT: Heterodimer of alpha and beta subunits; di
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
B5DA100D383E3547 CRC64;
                                                                                       Crotalus horridus horridus (Timber rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Botrocetin, alpha chain (Platelet coagglutinin).
                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CHH-B alpha subunit.
                                                                                                                                                                                                                                                                                            PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                   127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AA.
                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                15162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ECPSGWSSYDRYCYKPF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bothrops jararaca (Jararaca).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 70.6
                                  STANDARD;
                                                                                                                                                                                                                                                                                    SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                         121
15
120
81
                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                               127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8724;
                                                                                                                                                                                                                                                                                                                                   32
81
                                                                                                                                                      IISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993
15-SEP-2003
                                 CROHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOTA BOTJA
P22029:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Titani K.;
                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                 Lectin.
                       CHBA_CROHO
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             RESULT 4
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"Isolation and chemical characterization of two structurally and functionally distinct forms of botrocetin, the platelet coagglutinin isolated from the venom of Bothrops jararaca.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Two-chain Botrocetin forms an activated complex with vWF, and the complex then binds to platelet GPIb, resulting in platelet agglutination.
-!- FUNCTION: There are two distinct forms of the von Willebrand
                                                                                                                                                                                                                                                                                                                                                   'Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alboaggregin B beta subunit.
Trimeresurus albolabris (Mhite-lipped pit viper).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH C-75 IN BETA CHAIN)
                                                     Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
Fukui H., Sugimoto M., Ruggeri Z.M.;
                                                                                                                                                                                                                                                                  MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15215 MW; E4CF4502946AC74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRIAB
ABBB TRIAB
P8116,
18-10L-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
THR-2003 (Rel. 41, Last annotation update)
The subunit.
The subunit.
                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
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PDB; 11JK; 17-JUL-02.

PDB; 1EVU; 14-FEB-01.

InterPro; IPR002153; Antifreezell.

InterPro; IPR0031304; Lectin C.

PEAM; PF00059; lectin C; 1.

PRINTS; PR003156; ANTIFREEZEII.

SWART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
TISSUE=Venom;
MEDLINE=91129280; PubMed=1993206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
MEDLINE=98189535; PubMed=9531050;
                                                                                                                                                                                      Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DCPSGWSSYEGNCYKFF 17
                                                                                                                                                                                                                                                                                                                                                                                                     Structure 10:943-950(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 82.4 es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AA;
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RESULT 8
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                                        Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           platelets.";
Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.
                                                                    -!- SÜBÜNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
-!- SÜBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                      C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
INTERCHAIN (WITH C-79 IN ALPHA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                       Alboaggregin A subunit 3.

Trimeresurus albolabris (White-lipped pit viper).

Trimeresurus albolabris (White-lipped pit viper).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                  .
0
         Calvete J.J., Niewiarowski S.; "Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                             Length 118;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disulfide-linked.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                               f SIMILARITY.
059EDFF6B474C4CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAFA24C098DF3293 CRC64;
                                                                                                                                                                                                                                             Score 80; DB 1; 1
Pred. No. 5.9e-05;
                                                                                                                                                                                                                                                                                                                                                                           15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                  SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00615, C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                            125 AA
                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98189535; PubMed=9531050;
                                                                                                                                                                                                                 BY
                                                                                                HSSP, P23807; 11XX.
InterPro; IPR001304; Lectin C.
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P23807; 1IXX.
InterPro; IRR01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                 DCPSDWSSYDLYCYKVF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AA; 14798 MW;
                                                                                                                                                                                                                          13794 MW;
                                                                                                                                                                                                                                             74.1%;
                                                                                                                                                                                                                                                                                     1 DCPSEWSSYEGFCYKPF
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
15
121
113
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13
75
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                                                                                                                                                                                                                         118 AA;
                                                                                                                                                                                                                                                     Local Similarity
ses 12; Conserv
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98 4 4 3
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                              platelets."
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P81113;
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SEQUENCE
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TISSUE=Venom;
MEDLINE=91129280; PubMed=1993206;
MEDLINE=91129280; PubMed=1993206;
Pujfwura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
Fukui H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical characterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
Biochemistry 30:1957-1964(1991).
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure 10:943-950 (2002).
-!- FUNCTION: Two-chain Botrocetin forms an activated complex with vWF, and the complex then binds to platelet GPIb, resulting in platelet agglutination.
-!- FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain Botrocetin in promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH C-80 IN ALPHA CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
115-SEP-2003 (Rel. 42, Last annocation update)
Botrocetin, beta chain (Platelet coagglutinin).
Bothrops jararaca (Jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vWF binding to platelets.
-!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
vWF and Botrocetin form a soluble complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93157385; PubMed=8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
      Length 125;
                                                                    3; Indels
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-!- SIMILARITY: Contains 1 C-type lectin family domain.
Score 80; DB 1; I
Pred. No. 6.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                      125 AA
                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viperidae, Crotalinae; Bothrops
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                  17
                                                                                                                                                                                             3 DCPFGWSSYEGYCYKVY 19
   74.1%;
70.6%;
                                                                                                                                  1 DCPSEWSSYEGFCYKPF
      Query Match
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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PDB; IIJK; 17-JUL-02.
PDB; IFVU; 14-FEB-01.
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                                                                                                                                                                                                                                                                                                          Thromb. Haemost, 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                              Gaps
                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 1.
Trimeresurus albolabris (White-lipped pit viper).
Trimeresurus, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trimeresurus flavoviridis (Habu).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IXA_TRIFL
PR3806, 091246;
01-00-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor IX/factor X-binding protein A chain precursor
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0
                                                                                                                                                                                                                                                                                          "Alboaggregins A and B. Structure and interaction with human
                         73.1%; Score 79; DB 1; Length 125; 70.6%; Pred. No. 8.8e-05;
                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                                                                                                                                                                           MEDLINE=98189535; PubMed=9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.1%; Score 79; DB 1; Length 131
64.7%; Pred. No. 9.1e-05;
"Mismatches 2; Indels
                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                disulfide-linked.
-!-SUMERLUULAR LOCATION: Secreted.
-!-SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; p23806; 11XX.
       15037 MW; 1ED2027ED817FCA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3569F5BF91F6624 CRC64;
                                                                                                                               131 AA.
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BY SIMILARITY.
BY SIMILARITY.
                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR001304; Lectin_C.
                                                              1 DCPSEWSSYEGFCYKPF 17
                                                                         1 DCPPDWSSYEGHCYRFF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA; 15427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DCPSEWSSYEGFCYKPF 17
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            129
13
127
      125 AA;
                                  Local Similarity
Les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                       NCBI_TaxID=8765;
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98
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P81111;
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       SEQUENCE
                          Query Match
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Best Local
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IXA TRIFL
IX D IXA T
AC P2380
DT 01-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of C-type lectin domains.";

Nat. Struct. Biol. 4:438-441(1997).
-!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHICMBERY.
-!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                       MEDLINE=96184662; PubMed=8645314;
Mateuzaki K., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
"DDMA cloning of IX/X.BP, a heterogeneous two-chain anticoagulant
protein from snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97331317; PubMed=9187649;
Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COAGULATION FACTOR IX/FACTOR X-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                   Atoda H., Hyuga M., Morita T., "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH C-98 OF B CHAIN) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homology with asialoglycoprotein receptors, proteoglycan core
protein, tetranectin, and lymphocyte Fc epsilon receptor for
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
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                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 220:382-387(1996).
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InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; pancreatis ac.
Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SWART; SW00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS06041; C_TYPE_LECTIN 1; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91332000; PubMed=1831197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D83331; BAA11887.1; -. PIR; JC4690; JC4690.
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102
1242
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111
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                                                                                                                    SEQUENCE FROM N.A.
                                                      NCBI_TaxID=88087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin E
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0
                                                                                                                                                                                                                                                                                                                                     Gaps
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BY SIMILARITY.
INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
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INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crotalus durissus terrificus (South American rattlesnake).
Makaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes; Colubroidea,
Viperidae, Crotalinae, Crotalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. J. 333:389-393(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor, glycoprotein VI (GPVI).
-!- SUBUNI: Heterohexamer of three alpha chains and three beta chains; disulfide-linked.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145
                                                                                                                                                                                                                                                                           70.4%; Score 76; DB 1; Length 152; 76.5%; Pred. No. 0.00029; ive 0; Mismatches 4; Indels
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94D7E3E1BC693B9F CRC64;
                                                                                                                                                                                                                       17213 MW; FB3DDD2369009263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Convulxin beta precursor (CVX beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P23807; 1IXX.
InterPro; IPR001304; Lectin_C.
Pfam; PF000159; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00015; CTYPE LECTIN_1; 1.
PROSITE; PS00041; C_TYPE LECTIN_1; 1.
Lectin; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                     1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DCLSGWSSYEGHCYKAF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 AA; 17402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y16349; CAA76182.1; -.
                                                                                                                                                                                                                                                                                                     Local Similarity 76.5
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                   132
                                                                                                                                                                                                                       152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVXB_CRODU
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SEQUENCE
                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                       SEQUENCE
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                       HELIX
STRAND
HELIX
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STRAND
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rhodocetin alpha subunit.
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                               Wang R., Kini R.M., Chung M.C.M.;
"Rhodocetin, a novel platelet aggregation inhibitor from the venom of Calloselasma rhodostoma (Malayan pit viper): synergistic and noncovalent interaction between its subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 38:7584-7593(1999).
-!- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.
-!- SUBUNIT: Heterodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit disulfide bridges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=15955.90; MW_ERR=1.44; METHOD=Electrospray.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                              Gaps
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              Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 133;
                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386EAC519DFC674D CRC64;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABBA_TRIAB STANDARD; PRT; 132 AA. P8115; E-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Alboaggregin B alpha subunit.

Trimeresurus albolabris (White-lipped pit viper).
              Score 74; DB 1; | Pred. No. 0.00054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.00095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 72; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SMO004; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                   133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99303998; PubMed=10360956;
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              68.5%;
                                                                                                        27 CPSHWSSYDRYCYKVF 42
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Query Match
Best Local Similarity 68.0.
Thes 11; Conservative
                                                                           2 CPSEWSSYEGFCYKPF
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nes 10; Conservative
                                                                                                                                                                                   STANDARD;
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127
119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom;
                                                                                                                                                                                   RHCA AGKRH
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                                                                                                                                                     RESULT 12
RHCA_AGKRH
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us-09-938-114-4.rsp

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Pfam; PF00059; lectin_c; l. SMART; SM00034; CLECT; l.
 [3]
CHARACTERIZATION.
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P81398;
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                                                                                                                                                                                                                    Lectin.
DOMAIN
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RHCB_AGKRH
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                                                                                                                 Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.
                                                                                                                                                   -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amino acid sequence of the alpha subunit and computer modelling of the alpha and beta subunits of echicetin from the venom of Echis carinatus (saw-scalad viper).";
Blochem. J. 323:533-53(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97250657; PubMed=9163349;
Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Saqi M.S.A.,
Clemetson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Echis carinatus (Saw-scaled viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
INTESCHAIN (WITH C-75 IN BETA CHAIN)
(BY SIMILARITY).
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0
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                      TISSUE=Venom;
MEDIINE=98189535; PubMed=9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Nawiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                 63.9%; Score 69; DB 1; Length 132; 60.0%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                            -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                             C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
6FAE64820383F16F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AA.
                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                 HSSP, P23806; IIXX.
InterPro; IPR001304; Lectin_C.
Pfam, PR00059; lectin_c; 1.
SMART; SMO0034; CLECT, PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95091801; PubMed=7999097;
                                                                                                                                                                                                                                                                                                                            132 AA; 15419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viperidae, Viperinae, Echis.
NCBI_TaxID=40353;
                                                                                                                                                                                                                                                                                                                                                                                            1 DCPSEWSSYEGFCYK 15
                                                                                                                                                                                                                                                                                                                                                                                                        ||||:|||:
|CPSDWSSFKQYCYQ 15
                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                             129
13
127
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Echicetin beta subunit.
                                                                                                                                                                                                                                                                                                                  119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom;
                                                                                                            platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECHB ECHCA
                                                                                                                                                                                                                                                                                                                 DISULFID
SEQUENCE
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                                            SEQUENCE
                                                                                                                                                                                                                                                    Lectin.
                                                                                                                                                                                                                                                              DOMAIN
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ECHB ECHCA
                                                                                                                                                                                                                                                                                                                                                                       Matches
  qq
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Rhodocetin beta subunit.
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
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"Rhodocotin, a novel platelet aggregation inhibitor from the venom of Calloselasma rhodostoma (Malayan pit viper): synergistic and noncovalent interaction between its subunits.";

Biochemistry 38:7584-7593(1999).

-!- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.

-!- SUBUNIT: Hererodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disulfide bridges.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=15184.53; MW ERR=2.74; METHOD=Electrospray.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
MEDLINE=9324424; PubMed=8481512;
Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby B.P.;
"Echioetin: a snake venom protein that inhibits binding of von
Willebrand factor and alboaggregins to platelet glycoprotein Ib.";
Blood 81:2321-2328(1993).
-I- FUNCTION: Binds to platelet GPIb and inhibits platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.0%; Score 67; DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                             -1- SÜBÜNIT: Heterodimer of alpha and beta subunits.
-1- SUBCELLUIAR LOCATION: Secreted.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C42COAD7CDE18CA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.0047;
3; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99303998; PubMed=10360956;
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NCLPDWSVYEGYCYKVF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DCPSEWSSYEGFCYKPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
13
119
75
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Search completed: December 8, 2003, 09:53:10 Job time : 2.56762 secs

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RESULT 2
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Q91am0 agkistrodon
Q9def8 agkistrodon
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
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1: Sp_archea:*
2: Sp_bacteria:*
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Q98SM5
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1 DCPSEWSSYEGFCYKPF 17
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                                                                                          PRELIMINARY;
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
REMBLA AF176421; AAF26287.1;
REMBLA AF176421; AAF26287.1;
RESPECTABIOTY INTRAFF.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Rema; PF00059; Jectin_c; 1.
REMATY; SM00134; CLECTIN_2; 1.
REMATY; SM00134; CLECTIN_1; 1.
REMOSITE; PS00041; C_TYPE_LECTIN_2; 1.
REMOSITE; PS00041; C_TYPE_LECTIN_2; 1.
REMOSITE; PS00041; C_TYPE_LECTIN_2; 1.
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Zhmitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF35034; AAK26430.1; -.
HSSP; P23807; IIXX.
InterPro; IPR001304; Lectin C.
Emm; PR00059; lectin C; 1.
SWART; PR00059; lectin C; 1.
PROSITE; PS50041; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
SRQUENCE 124 AA; 14701 MW; 46B2D5E0CB3DC518 CRC64;
                 01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
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TISSUE=Venom gland;
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Ogawa T., Deshimaru M., Fukumaki Y.,
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TISSUE-Venom gland,
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TISSUE-Venom gland,
A Tani A., Nose T., Nikandrov N.N., Ogawa T., Deshimaru M., Fukumaki Y. Tani A., Nose T., Nikandrov N.N., Ogawa T., Deshimaru M., Fukumaki Y. Tani A., Nose T., Shimohigashi Y., Ohno M.;
The Chang C., Shimohigashi Y., Ohno M.;
The Tricoagulant protein from Deinagristrodon actus venom gland.";
The Submitted (JAN-22000) to the EMBL/GenBank/DDBJ databases.
The Submitted (JAN-22000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                        Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Delnagkistrodon.
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B chain of ACF 1/2 from Deinagkistrodon acutus.";
"B chain of ACF 1/2 from Deinagkistrodon acutus.";
"B chain of ACF 1/2 from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY091761; AAM22789.1;
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
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PRINTS; PR01504; PNCREATITSAP.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C TYPE LECTIN 1; 1.

PROSITE; PS0041; C TYPE LECTIN 2; 1.

SEQUENCE 146 AA; 16925 MW; F2493CACBASD2144 CRC64;
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01-OCT-2002 (TrEMBLrel, 22, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                Last sequence update)
Last annotation update)
146 AA
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TISSUEs-venom gland;
MEDLINE=99443731; PubMed=10512747;
Chung C.H., Au L.C., Huang T.F.;
"Molecular cloning and sequence analysis of aggretin, a collagen-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aggretin beta chain (Fragment).
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma)
                                 Gaps
                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                           Halyxin B-chain precursor.
Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Calloselasma.
NCBI_TaxID=8717,
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       90.7%; Score 98; DB 13; Length 146; 88.2%; Pred. No. 2.7e-07; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                TISSUB=Venom;
Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
"A Novel Coagulation Factor Xa Inhibitor from Korean Snake
                                                                                                                                                                                                                                                                                                                                  (Agkistrodon halys) venom.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF197915; AAG28522.1; -.
HSSP, P23807; LIXX.
INTEFPO; IPRR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HALYXIN B-CHAIN.
C47D8A43B0A00709 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                      146 AA
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                                                                                                                                                                                                                                                                                                                                                                                                    PEAM, PF00059; lectin c; 1.
PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
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SEQUENCE 146 AA; 16841 MW;
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                                                      1 DCPSEWSSYEGFCYKPF 17
                                                                            24 DCPSDWSSYEGHCYKPF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DCPSEWSSYEGFCYKPF 17
        Query Match
Best Local Similarity 88.2
Matches 15, Conservative
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                                                                                                                                      PRELIMINARY;
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Q91840
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Wang W.-J., Ling Q.-D., Huang T.-F.; "Molecular structure and functional characterization of agglucetin, a tetrameric glycoprotein ID-binding protein, from Formosan pit viper."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang W.J., Huang T.F.;
"A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist.";
Thromb. Haemost. 86:1077-1086(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
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88.2%; Pred. No. 1.1e-06;
ive 0; Mismatches 2; Indels
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88.2%; Pred. No. 1.5e-06;
tive 0; Mismatches 2; Indels
                                                                                    TISSUB=Venom gland;
Chung C.H., Au L.C., Huang T.F.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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24 146 AGGLUCETIN-BETA 1 SUBUNIT.
146 AA; 16728 MW; 2342BAE38EBOCCB9 CRC64;
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146 AA; 16770 MW; 930839140CFD8908 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
platelet aggregation inducer.";
Biochem. Biophys. Res. Commun. 263:723-727(1999)
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                                                                                                                                                                                                                                                  Pfam; PF00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                      EMBL, AF244901, AAF79953.1; -. HSSP, P23807; 1IXX.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003999; Pancreatis_ac.
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hes 15; Conserv
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Matches 15; Conserv
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SEQUENCE
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QBAYA4;
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Q9Y192;
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Q9YI92
ID Q9YI9AC Q9YI
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MEDLINE=93326575; PubMed=8334120;
Sekiya F., Atoda H., Morita T.;
"Isolation and characterization of an anticoagulant protein homologous
to botrocetin from the venom of Bothrops jararaca.";
Biochemistry 32:6892-6897(1993).
                                                                                                                                                                                                           SEQUENCE FROM N.A.
Kim D.S., Koh Y.S.;
"Purification and molecular cloning of snake venom fibrin clotting
                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84; DB 13; Length 145; Pred. No. 3.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%; Score 81; DB 13; Length 30; 70.6%; Pred. No. 2.2e-05; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                        inhibitor.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      PEAM, PP00059, lectin c; 1.
PRINTS, PR01504, PNCREATITSAP.
SMART, SM00034, CLECT; 1.
PROSITE; PSS0041, C_TYPE LECTIN 1; 1.
PROSITE; PSS0041, C_TYPE_LECTIN 2; 1.
SEQUENCE 145 AA, 16746 MM; 6FFC67E2CIF20BCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Factor IX/factor X binding protein B chain (Fragment).
                                                                   Agkistrodon halys brevicaudus (Korean slamosa snake)
brevicaudus).
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SEQUENCE 30 AA; 3506 MW; 14A2DFFE41F2B6F5 CRC64;
        01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Fibrinogen clotting inhibitor B chain.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
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InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
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82.4%;
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ID Q9DEF9
AC Q9DEF9;
DT 01-MAR-2
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Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
Suzuki M., Matsui T., Titani K., Yoshioka A.;
Suzuki M., Matsui T., Titani K., Yoshioka A.;
"The cDNA cloning and molecular characterization of a snake venom
platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
halys bromhoffii venom.";
Thromb Haemost. 79:1199-1207(1998).
EMBL; AB019616; BAA34425.1; --
HSSP; P23807; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
MEDLINE=93326575; PubMed=8334120;
Sekiya F., Atoda H., Morita T.;
Sekiya F., Atoda H., Morita T.;
"Isolation and characterization of an anticoagulant protein homologous to botrocetin from the venom of Bothrops jararaca.";
Biochemistry 32:6892-6897(1993).
HSSP; P23807; 1IXX.
SEQUENCE 30 AA; 3709 MW; DD49A218EDDBA9D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                   Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Depidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Agkistrodon.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Bothrops.
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR01334; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
SEQUENCE 146 AA; 17064 MW; FEDAB4BDCC24E76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Factor IX/factor X-binding protein A chain (Fragment).
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.6%; Score 86; DB 13; L. Best Local Similarity 76.5%; Pred. No. 1.7e-05; Matches 13; Conservative 2; Mismatches 2;
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nes 13; Conservative
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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A Gawa T., Tani A.,

A Gawa T., Tani A.,

Anticoagulant Protein from Agkistrodon actus Venom Gland.";

L Submitted (JAN.2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB013680; BAA99281.1;

R HSSP; P23806; JIXX.

R HSSP; P23806; JIXX.

R InterPro; IPR001304; Lectin_C.

R FSMART; SM00059; Lectin_C.

R PROSITE; PS000615; C TYPE LECTIN_1; 1.

R PROSITE; PS000615; C TYPE LECTIN_2; 1.
                                                       Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
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"A chain of ACF 1/2 from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AMA22786.1;
InterPro; IPR001304; Lectin.C.
InterPro; IPR00399; Pancreatis_ac.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.

PROSITE; PS00061; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

SRQUENCE 152 AA; 17108 MW; B0870F3DA0A4D23B CRC64;
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152 AA; 17124 MW; 5C59C0F503A4D223 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                           Anticoagulant protein A precursor.
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RESULT 15

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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                        Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
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                                                                                                                                                                                                                                  Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.,
"A novel coagulation factor Xa inhibitor from Korean snake
(Agkistrodon halys) venom.",
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF190827; AAG17178.1,
HSSP; P23806; 1IXX.
InterPro; IPR001394; Lectin.C.
InterPro; IPR0013990; Pancreatis_ac.
Pfam; PF00059; lectin.c; 1.
PRINTS; PF01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN 24 152 HALYXIN A-CHAIN.
SEQUENCE 152 AA; 17455 MW; BDD74DIDC280C28D CRC64;
                           (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PRT;
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                                                                        Halyxin A-chain precursor.
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Best Local Similarity 76.55
Matches 13, Conservative
PRELIMINARY;
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

December 8, 2003, 13:34:19; Search time 440.543 Seconds (without alignments) 937.879 Million cell updates/sec Run on:

US-09-938-114-4 108 1 DCPSEWSSYEGFCYKPF 17 score: Sequence: Title: Perfect

BLOSUM62 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext Scoring table:

22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

Command line parameters:
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-MODEL=frame+ p2n.model -DEV=x1h
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-DE=C=Cqn2 1/USFTC_spool/US0938114/runat_08122003_091000_22859/app_query.fasta_1.725
-DE=EST_CFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DETATR=1 - EXD=-1 - MATRIX=blosum62 - TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 - ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLER=200000000
-USRE-SCO9938114 @CGN 1 1 4382 @runat 0812203 09100 22859 -NCFU=6 -ICPU=3
-NO MMAP -LARGEGUERY -NEG SCORES-0 -WAIT -DSPBICK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query	Query	2	£	יייייייי אינייייייייייייייייייייייייייי	
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37	62	57.4	m	13	609	5090	
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ALIGNMENTS

linear EST 01-MAY-2002

BM401696 172 bp mRNA linear EST 01-MAY-2 PHIA01F Snake Bothrops insularis library IL2 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence. BM401696 BM401696.1 GI:20376324 ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION BM401696 RESULT 1

Bothrops insularis (island jararaca)
Bothrops insularis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops

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/tissue_type="venom glands"
/clone_lib="Stanke Bothrops insularis library IL3"
/clone_lib="Stanke Bothrops insularis library IL3"
/note="Organ: venom glands, Vector: pGEMIZE+; Site_l: Eco
RI; Site_l: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally clone in pGEMIZE+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
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JUICOTF Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

BM#01618
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1 (bases 1 to 378)
Unnqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

2021.239 (1-2), 279-291 (2002)
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                               Contract: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 722 ext. 2083
Fax: 55 11 37 26 1505
Bmail: hoplee@usp.br
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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/db_xref="taxon:8723"
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BM401618
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// (db_tref="texaon:8723"
/tissue type="venon glands"
/tissue type="venon glands"
/clone_lib="snake Bothrops insularis library IL2"
/clone_lib="snake Bothrops insularis library IL2"
/clone_lib="snake Bothrops insularis state of the library libe library IL2"
/note="Organ: venom glands, vector: postmitzf+; Site_library library librar
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343 bp mRNA linear EST 01-MAY-2002 JL2E04F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
1 (bases 1 to 172)
Judgeira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
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Contact: Paulo Lee Ho
Contact: Paulo Lee Ho
Contact: Datantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
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/tissue type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
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1 (bases 1 to 391)

Umqueira-de-Azevedo, L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences. The putative identification of each EST columner was obtained through Blast searches (e-value cont).
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Contro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL03A (see Reference)
Email: hoplee@usp.br
This BST corresponds to cluster BITL01A (see Reference)
Seq primer:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 others
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Bothrops insularis
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Matches:
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                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:8723"
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Best Local Similarity:
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/Lissue type="Venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Organ: venom glands; vercor: pGEM11Zf+; Site 1: BCo
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11Zf+ vector (Promeça). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
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BM401621.1 GI:20376249
EST.
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/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands, Vector: pGEMIL2f+; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
1 (bases 1 to 475)
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A survey of gene expression and diversity in the venom glands of the pituiper snake Bothrops insularis through the generation of expressed sequence tags (ESTB)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GATTGTCCCTCTGATTGGTCCCCTATGAAGGGCATTGCTACAAGCTCTTC 185
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Centro de Biotecnologia
Instituto Butanta in 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hople@quep.br
This BST corresponds to cluster BITLOIA (see Reference)
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Percent Similarity:
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//mol type="memba"
//mol type="memba"
//dob xref="taxon:8723"
//tiseue type="venom glands"
//clone lib="snake Bothrops insularis library IL3"
//clone lib="snake Bothrops insularis brocker:
//clone lib="snake Bothrops insularis library IL3"
//clone lib="snake Bothrops insularis brocker:
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cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11Zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
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Viperidae, Crotalinae, Bothrops.

J. (bassa I to 504)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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This EST corresponds to cluster BITL01A (see Reference)
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113
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Best Local Similarity:
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AUTHORS
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COMMENT

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/tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/clone library IL3
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Viperidae; Crotalinae; Bothrops.
Junqueira-de-Azevedo, I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
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Contact: Paulo Lee Ho
Contact: Paulo Lee Ho
Contro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
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Bothrops insularis
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Matches:
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/db_xref="taxon:8723"
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                                 113 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 c
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76.85$
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                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                     128 a
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us-09-938-114-4.rst

Query Match: DB:

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE PUBMED COMMENT

FEATURES

DEFINITION

ACCESSION

RESULT 8 BM401495 LOCUS

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/mol_type="mRNA"
//mol_type="mRNA"
//db xref="taxon:8723"
/tissue type="venom glands"
/tissue type="venom glands; vector: pGEMILZE; site_1: bco
note="Organ: venom glands; vector: pGEMILZE; site_1: Eco
IN; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with Oligo-(dT) and reverse
transcribed to cDNA using Superscript plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZE+ vector (Promega). ESTS
were generated from random clones and grouped in unique sequences. The putative identification of each EST or
                                                                                                                                     BM401520 374 bp mRNA linear EST 01-MAY-2002 JH2G02F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Bothrops.

1 (bases 1 to 374)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                              A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cluster was obtained through Blast searches (e-value e-05)."
  Contact: Paulo Lee Ho.
Centro de Bioteonologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This EST corresponds to cluster BITL06A (see Reference) Seq primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe
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Best Local Similarity:
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SOURCE
ORGANISM
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BM401552
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TITLE
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BM401520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Venom glands"
/clone_lib="Stake Bothrops insularis library IL3"
/clone_lib="Stake Bothrops insularis library IL3"
/note="Organ: venom glands, vector: pGEM12E+; Site_1: Eco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM12E+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or
                                                                                                                                                                                                                                                                                              BM401495 512 bp mRNA linear EST 01-MAY-2002 JH2B09F Snake Bothrops insularis library IL3 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 512)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

600-299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                     93 GATTGTCCCTCTGATTGGTCCCCCTATGAAGGGCATTGCTACAAGCTCTTC 143
                                                                                                                                                             1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Paulo Lee Ho Centro de Biotecnologia Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITLOIA (see Reference)
Seq primer: M13F.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Conservative:
Mismatches:
Indels:
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Bothrops insularis
                                                                  Gaps:
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/db_xref="taxon:8723"
                                                                                                                x BM401667 (1-510)
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1. .512
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                   Best Local Similarity:
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Pred. No.:
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EST 01-MAY-2002

17

BASE COUNT ORIGIN

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Similarity:
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Best Local Similarit
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                                                           REFERENCE
AUTHORS
TITLE
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MEDLINE
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COMMENT
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TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Gratiaties = "Decentary transcription | Creaming | Monitor | Lype="mRNA" | Monitor | Lype="mRNA" | Monitor | Lype="venom glands" | Library IL3" | Library IL3" | Loone | Libe="Nanke Bothrops insularis library IL3" | Loone = "Organ: venom glands; Vector: pGEM11Zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to conA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM12f+ vector (Promega). ESTS were generated from random clones and grouped in unique
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BM401620. GI:20376248
                                                                                                                          Eukaryota: Merazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria: Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.

J. (bases 1 to 497)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bochrops insularis through the generation of energy sequence tags (ESTE)
Gene 299 (1-2), 279-291 (2002)
JHJE12F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
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                                                                                                                                                                                                                                                                                                                                                        Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL06A (see Reference)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bothrops insularis"
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                                                                                              Bothrops insularis (island jararaca)
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Bothrops insularis
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                                     BM401552
BM401552.1 GI:20376180
                                                                                                                                                                                                                                                                                                                                              Contact: Paulo Lee Ho
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a 109 c
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76.47%
75.93%
                                                                                                                Bothrops insularis
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                                                                                        SOURCE
ORGANISM
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SOURCE
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 DEFINITION
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TITLE
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MEDLINE
PUBMED
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BM401620
                                     ACCESSION
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                                                       VERSION
KEYWORDS
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/u.s./o
/vorganism="Bothrops insularis"
/mol_type="mRNA"
/db_tref="taxon:8723"
/tissue_type="venom glands"
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/note="Organ: venom glands, Vector: pGEMI1Zf+; Site_1: Eco
RI; Site_2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEMI1Zf+ vector (Promega). ESTS
were generated from random clones and grouped in unique
sequences. The putarive identification of each EST or
cluster was obtained through Blast searches (e-value <
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JH1D06F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 460)
Junqueira-de-Azevedo,I.L.M. and Ho,P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauxia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 378)
                                                                                                            Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)
Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                                                                      Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butanto 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITLILA (see Reference)
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Matches:
Conservative:
Mismatches:
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us-09-938-114-4.rst

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AUTHORS
TITLE
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PUBMED
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                /tisue type="venoring glands"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library IL3"
/clone lib="Snake Bothrops insularis library LL3"
/note="Organ: venom glands; vercor: pGBM12E*; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGBM12E* vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putarive identification of each EST or cluster was obtained through Blast searches (e-value c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM401417 574 bp mRNA linear BST 01-MAY-2002 GH061F Snake Bothrops insularis library IL2 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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Lepidosauvia; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 574)
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A survey of gene expression and diversity in the venom glands of the pitutiper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
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                                                                                                        Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazili, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                      Email: hoplee@usp.br
This EST corresponds to cluster BITL13A (see Reference)
Seq primer: M13F.
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Bothrops insularis"
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Bothrops insularis
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
22347338
                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:8723"
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                                                                                                                                                                                                                                                                    Location/Qualifiers
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BM401417.1 GI:20376045
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Instituto Butantan
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                                                                                            Contact: Paulo Lee Ho
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DB:
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TITLE
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BM401417
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//db_tref="taxon:8723"
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/tissue type="venon glands"
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/clone_lib="Snake Bothrops insularis to close 
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1 (basea 1 to 654)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTS)

Gene 299 (1-2), 279-291 (2002)
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Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900 Tel: 55 11 37 26 7222 ext. 2083 Fax: 55 11 37 26 1505 Ext. 2083 Ext. 55 11 37 26 1505 Email: hoplee@usp.br This EST corresponds to cluster BITL10A (see Reference)
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Mismatches:
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/organism="Bothrops insularis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 C
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Best Local Similarity:
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/tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL2"
/clone lib="Snake Bothrops insularis library IL2"
/clone lib="Organ: venom glands; Vector: pGEMIJZF+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGBMIJZF+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM401686 633 bp mRNA linear EST 01-MAY-2002 PH015FB Snake Bothrops insularis library IL2 Bothrops insularis CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
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/db_xref="taxon:8723"
/tissue_type="venon glands"
/clone_lib="snake Bochrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEMILZf+; Site_1: Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazca, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viperidae, Crotalinae, Bothrops.

1 (bases 1 to 633)

Junqueira-de-Azevedo, L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of the pitroper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hople@usp.br
This BST corresponds to cluster BITLO2A (see Reference)
                                                                                                                                                                                                                                                                                                                                                                                                                 8 others
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12
3
3
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Matches:
Conservative:
Mismatches:
Indels:
                   /organism="Bothrops insularis"
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Bothrops insularis
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                                                                ="taxon:8723"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.00
82.35%
70.59%
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AUTHORS
TITLE
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PUBMED
COMMENT
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KEYWORDS
SOURCE
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completed: December 8, 2003, 17:24:34

Job time : 441.543 secs

Search

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RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for CDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pp) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11Z+ vector (Promega). BSTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 GATTGTCCCTCTGATTGGTCCCCTATGGAGGCATTGCTACAAGCTCTTC 132
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Matches:
Conservative:
Mismatches:
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70.59%
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Best Local Similarity:
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